

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCCGAGGACCTGGAGCTCCGGCTCGCTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGCTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGGTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGCTGACGGCTTCGAAGAAACG
GAAGATGCCGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTIONACCTTTAAATTATTTCAGAAGGATGTCC
CGTGGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTTGATATATTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAATC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTGCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACAGCTGTGGAATG
TGTGTCAAGTTAGGTTGTGGAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTL SKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LKVCSPGT YGPDCLACQGSQRPCSG
NGHCSGSGSRQGDGSCRCHMGYQGSLCTDCMDGYFSSLRNETHS ICTACDESKCTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKE C I SGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAAEAATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCGCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGGCTCGCCAGGCCGGGAGGCGACGCCGCCAGCCGCTTAAACCGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTTGCG
GCACGAGGAGTTTTCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCCGGAGGAGCGCCTTC
CTGCCCCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGACCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
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TTCAGAAAAAGCGCAACAGAGAAATGCCAGCTATTCTGTCAATATCCATTCCATGAAATTTTAC
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TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGAGCGCATCTGCGAGTGTCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTG
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GATTCATGAGAGTGAACGTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCTGGAATAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
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TGAACCTCCGACATCTGAACGTTTTAAGTTACACCAAGTTCTATAGCCTTTGTAAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTCTCTTTAAGTTTCTAAGTACGCTCTGTAG
CATGATGGTATAGATTTTCTTGTTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAATTTTTCAGTGTGTAGTTGGCAGATATTTCAAATAACAATGCATTTATGGT
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TTACCATATTCCAGAGATTCAATATTAACCAATGAAATAGGGAATATAATGTATGAACCTTTTGCAT
TGGCTTGAAGCAATATAATATATTTGTAACAAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAGGCTTGGC
CGCCATGGCCCACTTGTTTATTCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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GTVPFKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNITLQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGHPCAKLCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKICPPGLEGEQCEISKCPQPCRNGGKIGKSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHPNKCQCQEGWGHRCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGGTAC
TGCTGTGTGCTGCCGTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGTCTGCCCTGACTTCTGGGACTTC
TGCTTCGGCGTGCCACCCCTTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACCTGTAAACGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCTGGATTGAGGGCATTTCGTACCGCCTGGGCACCA
TCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGTCTGAACCCAGGGGAG
GTGCTTCCCACAGCCTTCGAGGGCTCTGAGAAGTGGCCCAACCTGATTTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCAAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCGAGAACCTGCTGTCTTGTGAC
ACCCACAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTCTCTGCGTGC
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTTCGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
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CGGGCACCACGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGCGCTAAT
CCGGCGCGGGTTCGCTGACGCGAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGCGC
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGGAGTGCACTGGCCATCAGGGCTCACTGAACCTCCGACTCCTGGGTTCA
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACACACACCTGGC
TAATTTTTGTATTTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDGP
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTAACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCACACTGGGTGTGGTGCCCCAGGCCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCCTGCAGATGGCCCCCTCCAACCCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTTAACCCGTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCCTGGAGGAA
GGGGCCAGGCCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVVPQASVPLLTDLAQWEPVLVPEAHFNASLTMYVCTPVPHDPPMALSRTPTRQISSSDT
DPFADGFSNPLCCCFHGPAFSTLNPVLRHLFPQEAFFAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCTGCTGCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGCGAGCCGGTTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCAGAACGCCCGGCACGAGG
GCTGTTTCATGGCCTTCACGCGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCAACACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGGCCGCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTTTGTTTGTTCAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCCTGCACCCACCCCCAACTCCAGCCC
CGGAATAAAACCATTTTCTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTTEIVLE
NNYTAFQNAHHEGWFMATFRQGRPRQASRSRQNRQEAHFIRKLYQGQLPFPNHAEEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTTGATTTGCTGTTTATTTTTTTTTCTTTTTCTTTTCCCACCACATTGATATTTTAT
TTCCGTACTTCAGAAATGGGCCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCTCT
GAAGTCTTGGCTTATCAITTCCTCTGGGGCTCTACTCACAGGTGTCCAAACTCTCGGCCGTGCC
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CAITTTGTGAATGATACTTCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGTATGGCATA
CAAACCTCACATGGGTGAAAAATGGGCCACAGTTTGTAGTGGGGGCATGTTGAGGAGCGCATAG
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CACCACCATGCTCTCTATCTGAACAACGGCAGCAACACAGGCTCCAGCCATGAGCAGACGA
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TTGTGCAATTTGAATCTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTTCTATTCAAGTTAATTACAAACAGTTTTGTACTCTTTGCTTTTTAAATCTT

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FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRNDFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPNMLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAI SLKLLPLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDI SNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSI KWVTEWLKYIPSSLNVRGFMCGQPEQVRGMAVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPI SERIQLSIHFNVD
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHL SLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASLYLNNGSNTASSHEQTTS HSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETS FQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHI PNNMRYCNSSVPPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGCGGAGACAGAGGCGAGAGCGAGAAGCTGGGGCTCCGTCCTCGCCTCCACGAGCG
 ATCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGCCGACGAGGAAGACCCGGGTGGCTCGGCCCTGCC
 TCGCTTCCAGAGCGCGCGGCTGCGAGCCTTGCCCTCTTGCTCGCCTTGAAATGAGAAAGATGCTGCGAGGCT
 GCTTTCTGCTGATCTCTGAGACAGATGTCCTCTCCCTGCCGAGGCCGAGGACGGGTCACTGGGAGGTTCATCT
 CTAGGGGCGACACCGCTCGGACCCACCCGACAGCGGCCCTTCTGGAGAGTCTCTGTAGAAACAAGCGGCGACCC
 TGGTTTTCATATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTCATCTGGACA
 TCTTGCAATTCTTGGACATTTGGTCTTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCAGCTGTCAAGAATG
 AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTCTGTCTCAAGAGGATGGCGCATCTGTCCAGG
 GCACCATGATCTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATCTCAGAGAGCGATGGCGCATCTGTCCAGG
 GGGAGATGTGCCAGCGGTCTAATATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGGTGCTA
 AGCCACGGGACACCGGATCTCTAATCTTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
 GAGGTGAGACCCCTGAGGACATGTCTCTGTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
 AGAAGAAGTGTGTGACGCGCCACATGTGACGACCCCTGGAGCATAAAGTGTGCCCACTTGTGCATCAACATCCCTG
 GCTCATACGCTGCGAGGTGCAACAAAGGCTACATCTCAACTCGGATCAGACGACTTGACGAATCCAGGATCTGT
 GTGCCATGGAGGACACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCCTTCGTCTGCCAGTGTCTACAGTG
 GCTAGCGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGACTACTGTGCCCTGAGAAACACCGGATGTGAAC
 ATGAGTGTGTAATGTGTGATGGTCTCTAACCCTTGGCCAGTGGCATGAAGGATTGTCTTAAACCCAGATGAAAAA
 CGTGCAACAGGATCAACTACTGTGCACTGAACAAACCGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
 ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACTGCAGCCGATGGACCACTGTGCAC
 AGCAGGACCATGGCTGTGAGCAGCTGTGTGAAACACGGAGGATTCCTTCGTCTGCCAGTGTCTCAGAAAGGCTCC
 TCTCAACGAGGACCTCAAGACCTGTCTCCGGGTGGATTACTGCTGCTGAGTGACCATGGTTGTGAATACTCCT
 GTGTCAACTGGACAGATCTTTGCTGTGCTGCTGAGGGACAGTGTCTCGCAGCGATGGGAAGACGTGTG
 CAAAATTTGGACTCTTGTGCTCTGGGGACACGGTGTGAACATTCGTGTGTAAGCAGTGAAGATTCTGTTGTGT
 GCCAGTCTTTGAAGGTTATATACTCCGTGAAGATGGAAGAACTGCAGAAAGGAAGATGTCTGCCAAGCTATAG
 ACCATGGCTGTGAACACATTTGTGTGAACAGTGAAGACTCATACAGTGCAGTGTCTTGGAGGGATTCGGGCTCG
 CTGAGGATGGGAACGCTGCCGAAGGAAGGATGTCTGCAAACTCAACCCACCATGGCTGCGAAGACCATTTGTGT
 ATATGGGAATTCCTACATCTGCAAACTGCTCAGAGGGATTGTGTTAGCTGAGGACGGAAGACGCTGCAAGAAAT
 GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAGGAATTTTGAGGTCG
 TGAAGCAGTTTGTCACTGGAATTATAGATTCTCTGACAATTTCCCCAAAGCCGCTGAGTGGGGCTCTCCAGT
 ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCACTCAGCCAAAGACATGAAAAAAGCCGTGCCCC
 ACATGAAATACATGGGAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGGAGAGAATTTTACCAGG
 GAGAAAGGGCCAGGCCCTTTCCACAAAGGTTGCCAGAGCAGCCATTTGTGTTCAACGACGGACGGCTCAGSATT
 ACGTCTCCGAGTGGGCGAGTAAAGCCAAAGGCCAATGGTATCACTATGTATGCTGTGTGGGTAGGAAAGCCATG
 AGGAGGAACACAAAGAGATTGCTCTGAGCCCAACAAAGCATCTCTTCACTGCCGAAGACTTCAGACAAATGG
 ATGAGATAAGTGAAGAACTCAAGAAAGGCATCTGTGAAGCTTAGAGAGCTCCGATGGAGACAGGACTCTCCAG
 CAGGGGAACCTGCCAAAGCCGCTCCACAGCCCAACAGAACTGTGAGCCAGTCAACATAAATACCAAGACTACTTT
 CCTGTCTCAATTTTGCACTGTCAACACAGATATCTGTTTGAAGAGACAACTTTTACCGTCTACACAAAGCTTT
 CCCATCTCAACAAACCTTCAGGAAGCCCTTTGGAAGAAAAACAGATCAATGAGTCAATGAGAAACCTTATAATG
 TCCAGAACCTTTGCAACCGAAGATGAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC
 TGGAAATTCGCTGAGATACAGATGAAGATTAGAAATCGGACACATTTGTAGTCTTGTATCAGGATTACAAAT
 GAACCGAGTGCAGAGCCCAAAGCTCAGGCTATTGTTAAATCAATATGTTGTGAAGTAAACCAATCAGTACTGA
 GAAACCTGGTTTGGCCAGAAACAAAGACAGAAGGTATACATACTTGTATATAATTTACTAGGAAAAAAATCC
 TCAAGATCTTAAGATTGAATTTACCAAGGTGAGAATGAATAAGCTATGCAAGGTAATTTGTAAATATATCTGTGGACAC
 AACTGTGCTTCTGCTCACTCTGCTAGTGTGCAATCTCATTGACTATACGATAAAGTTTGCACAGTCTTACTT
 CTGTGAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGACCTTACCTTGATATATGTATATGGATGTATG
 CATAAATCATAGGACATGTGATTTTGGGAACAAGTTGGATTTTTATACAAATTAATAATTCCACCTCTAG

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FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KRMRLHSLGTMTGLAIQYALNIAFSEAEGARPLRENVPVIMIVTDGRPDQSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASNHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINRYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSPACQCEGHVLRSDGKTC AKLDS CALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCCQALDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKLHLYAEDFSTMDEISEKLKGI CEALSDSDGRQDS
PAGELPKTVQQPTESEPTVINIQDLLSCSNFAVQHYRLFEEENLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFONLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCCTGGTGACCAAC'TGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGTACACCTTGCACGGGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAA CAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAATCAATGTACTGGTTCCTCCAGTCCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGGCAAACTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACAGCATTAGATGTCTATCCGTG
GGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGTCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTTC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGACCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCTCTGTCTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGCAT
TGACCCCAACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAGACTGCCACACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATGAAGTAC
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCCATATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACTATCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGGCAGAGACTTCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCCATCCAGCTCAGCTCCCTGT
ATTGATATAACCTGTGAGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAACATGAAATATGTGTGTTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQWEVFPVMWFFKQKEKEDQVLSYINGVTTSTKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFPAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLFPWPKSSDTISKNGTL
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPISIPGGVSSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAAATGAACGCGCTCCCGCTCCTAGTGGTTTTTTCACCTTTG
TTGAATTGTTCTTACTCAAAATTGCACCAAGACACCTTTGTCTCCCAAAATGC AAAATGTGA
AATACGCGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTACAA
TTTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGTCCTGTGGCGAAAAATGCTAATTGTC
ACTAACACAGAAGGAAGTTATTATGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTTATCACTAATGATGGAACCGCTCTGTATAGAAAATGTGAATGCAAACTGGCCATT
TAGATAATGTCTGTATAGCTGCAAAATATTAATAAACTTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAGAAAGTCTATAGAAATCTGTGACAGATCTTTTACCACACAGA
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACACA
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTTGAT
TCATATAACATGAAACATATTTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCTTTTCTTCATCATCTGACAACTTCTTATTGAAAGCTCAAAATTTATGAT
AATCTCAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATGAACCTGAAAAAATAACATTTACATTTAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGCTCATATGTGCATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGCATACTCAAATGAGACCCACACCTCATGCCGTGTAATCACCT
GACACATTTTGAATTTGATGTCCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTTCCTACTGATTTGTCTTGCCATGTCATTTT
ACCTTCTGGTTCTTCAGTGAAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
TAGCCTATTTCTTGCTGAACCTGTTTTTCTTGTGGGATCAATACAAATACAAATAGCTCT
TCTGTTCAATCATTTGCCGACTGCTACACTACTTCTTTTTCAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCTACTACAACAAGGGATTTTGTCA
CAAGAATTTTATATCTTTGGCTATCTAAGCCACAGCCGGTAGTTGGATTTTCGCGAGCAC
TAGGATACAGATATTATGCGACAACCAAGATATGTTGGCTTAGCACCGGAAAACAACCTTTAT
TGGAGTTTATAGAGCACAGCATGCCTAATCATCTTGTGTTAATCTCTTGGCTTTTGGAGTCAT
CATATACAAAGTTTTTTCGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAAC
TAAGGTCTGTGCAAGAGGAGGCCCTCGCTCTTCTGTTCCCTCTCGGCACACCTGGATCTTT
GGGGTTCCCATGTTGTGTCACGCATCAGTGGTTACAGCTTACCTCTTCAGCTCAGCAATGC
TTTCCAGGGGATGTTCAATTTTATTCTGTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAGATGCCCTGTTGTTTGGATGTTAAGGTAAACATAGAGAAATG
GTGGATAATTACAACCTGCACAAAAATAAAATTCGAAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAAATTCCTAATTTAATACTAGACAAAAAGTATTTTAAATCAGTTTCTTCT
GTTTATGCTATAGGAATCTGAGATAAAGGTAAATTTAGTATCATATAGATATACTATGT
TTTTCTATGTGAAATAGTTCTGTCAAATAAGTATTGTCAGATATTTGGAAGATAATTGGTTT
CTCAGGAGTGATATCACTGCACCAAGGAAGAGTTTCTTTTAAACACGAGAAGTATATGAA
TGCTCTGAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAACTAGTCC
CTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGAACATAAGAGAATGAAGGGGCAGA
ATATCAAACAGTGAAAGGGAATGATAAGATGTAATTTGAATGAAGTGTTTTTCTGTAGAC
TAGCTGAGAAATTTGTGACATAAAAAATAAGAAATTGAAGAAACACATTTTACCATTTTGTGAA
TTGTTCTGAAGCTTAAATGTCCATAAAACAACTTAGACTTCTGTTTGCTAATCTGTTTCTT
TTTCTAATATTCTAAAAAATAAAAGGTTTACCTCCACAATTGAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTIEGSSYYCMCVPGFRSSSNQDRFITNDGTVCIEVNNANCHLDNVCI
NINKTTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTLEFVKTVNNFVQRDTFVVWVDKLSVNHRRTHLTKLMHTVEQATLRISQSQFQKTTEFDT
NSTDIALKVFFDSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLKLPQNYDNSEEEBVISVSVSMSSNPPTLYELEKITFTLSHRKVTDTRYRSLCAF
WNYSPTDMNGSWSSBGCELTYSNETHTSCRCNHLTHFAILMSSGPGSIGIKDYNILTRITQLG
IIISLICLAICIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCISIAGL
LHYFFLAFAFWMCI BGIHLVLI VVGVIYNKGFLHKNFYIFGYLSPAVVVGFSALGYRYGYT
TKVCWLSTENNFIWFSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVASVVTAYLFTVSNAPQGMFIFLFLCVLSRKIQBEYYRLPKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTGTCTTGCCATATGCATTTTACCTTC
TGGTTCCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCGGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCCTCCCTCCCGCAGATCCGAACGGCCCTGGGGCGGGGTCACCCCGGCTGGGA
CAAGAAGCGCCGCGCTGCGTGC CGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCCTACTATATAAGGCTGCGCGGCCGGAG
CCGCCGCGCGCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCAGAGCCCCGACGCGATCCCGGTGCGCGCCAGGCCTCCCCGACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGCGTCCAGTATGG
ATCCTGGCCGCGCTCTGGCTGGCCGTGGCCGGGCGCCCTCGCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTTGCGCATCCGTGCCGACGGCGTCTGGACTGCGCGCGGGGC
CAGAGCGCGCACAGTTTGTGAGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACACAGCGTGGGTACCTCTGCATGGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTTCTGCCCATGTGCCCATGGTCCACAGGAGGCTG
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTCTTTCGCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT
GAGACCATGCCCGGCCCTCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTCTGTGTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCCTGGGCCCCCATCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATAACCTCCATCGATGGGGAAC
TCACTTCTTTGGAAAAATCTTATGTCAAGCTGAAATTTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCACAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATTCCCC
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTTGAGAATAACTTGCTGTCCGGTGTCACTGC
TTCCATCTCCAGCCCCACGACCTCTGCCCCACCTCACATGCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCCACCTTATGTCAACCTGCACCTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CGTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTCTTACATTATTTATGCCCCAAATTATATTTATGTATGTAAAGTGAGGTTTG
TTTTGTATATTAATAATGGAGTTTGTGTTGT

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FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSILLEIKAVALRTVAIKGVHVSRYLCMGADGKMQGLLOYSEEDCAFEE
EIRPDGYNVYRSEKHRLFPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCVEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGQSQT
NSSYTMNKTGTQLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFPQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGGAGGAGAAAGAG
 AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGACCTTGGCAT
 CATGCTGCTATTCTCTGCAAACTAGCAAGCATGGGATTAAATATTTTACTTCTAAATAA
 ATGAATTACTCAATCTCCTATGACCATTATACATACTCCACCTTCAAAAAGTACATCAATA
 TTATATCTTAAGGAAATAGTAACCTTCTCTTCTCCTCAATATGCATGACATTTTGGGCAATG
 CAATTGTTGGCACTGGCACTTATTTCAGTGAAGAAAAAATTTGTGGTTCTATGGCATTTCATCA
 TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCATCTGACTG
 TGGAACTCCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAAGTGAAGGACATGGCACT
 CCGAATTCATGTGCTACTTGGCCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTAT
 ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTTAACTTTCCAGCCAGATTGCC
 AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATTTGCAAAAAATGTAATCTCCACAG
 ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT
 ATTAATGTA AAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA
 ACTGCCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAGAATCTTATATTAATCACAAT
 TGCTTTCTCAAAATTTCACTGGAGCCTTTATTGGCTACATAAATCTTCTCGACTTCATCTC
 AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAGAGAT
 TCTGATGATTGGGGAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA
 ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
 GGACTGGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTGGATCTAAATAAAAAATCCTATTAATAGAA
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACAAACCTTAGATTGTCTTACATTCAACCCCAATGCATTTTTCAGACTCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
 CCAAACCTCAAGGAAATCAGCATACAGATTACCCCATCAGGTGTGACTGTGTCATCCGTTG
 GATGAACATGAACAAAACCAACATTCGATTATCATGGAGCCAGATTCTCCTGTTTTCGCTGGAC
 CACCTGAATTCACAGGTGAGAATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAATTTGT
 CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAGGCTGGAGCTATGT
 TTCTTTTCACTGTAGAGCTACTGCAGAACCAAGCCTGAAATCTACTGGATAACACCTTCTG
 TCAAAAACCTTTGCCTAATACCTTGACAGACAAGTTCTATGTCCATTCTGAGGGAACTACTA
 GATATAAATGGCGTAATCTCCAAAGAGGGGGTTTATATCAATCTGTATAGCAACTAACCTAGT
 TGGCGCTGAATTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAAGATAACATG
 GCTCTTTGAAATTTAAAAATAAGAGATATTCAGGCCAATTCAGTTTGTGTCTCTGGAAGCA
 AGTTCTAAAAATCTCAAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAAATCTCA
 TGCTGCGCAAGTGCTCGAATACCATTGATGTCAAGGTATATAATCTTACTCATCTGAATC
 CATCAACTGAGTATAAAATTTGTATTGATATCCACCATCTATCAGAAAAACAGAAAAATTA
 TGTGTAATGTCAACCAAGAGGTTTGACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
 CACAACCTATGGCCCTGCTTGGAGCCTTCTGGGGATTATGGTGTGATATGCTTATCA
 GCTGCCTCTCTCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
 AAACCAACCTTTGCAATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
 AGAAAAAGTACATCACTGAAAGTAAAAAGCACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVCPRCLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQLTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTTELPEKCLSELNQLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSIVIAGINLTEIPDNALVGLLENLESISFYDNRL
IKVPHVALQKVVNLFKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLDP
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPPEFQGNVRQVHFDRDMMEICLPLIAPESFPNLSNV
EAGSYVSFHCRTAEQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCATGTGTCTCCTCCTACAAAGTTTGTGTTCTTA
TGATACTGTGCTTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCCTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCCTAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTG CAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTTCCTCAATGCTGC
CAAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCACATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTGCCAACTGACTGTCTATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAACATTTGAA
ACTTTGTATTTTCAGTTTTTTTTTGAAATATGCCACTGCTGAACTTTAAACAAACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCCKGCLCSSSGGLNVTC SNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDC¹TLQQVLRSMASNHETAHNVIC²TSVLDEHAGR³PFL
NAANDADLCNLPKKT⁴TDYAMLVTMFGWFTMVISYVVYYVRQ⁵QEDARRHLEYL⁶KSLS⁷PSRQ⁸KK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTGTCAGGCTCGGGCCACGGGCTGCCGCCCGCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCGAGGGGCATCCCCACCGAG
ACGCGCCTGTGGACCTAGGCAAGAACC GCATCAAAA CGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCGAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAAC
TGCTCTTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGCTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCGAGAGATCCAGCTGGTGGGC
GGGCGAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCACTGACCACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCTCTGTTGGTGTTCGG
CGCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCGCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTTCACTTGC CGCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACCGGTGCAGT
GTGTGCCGGGCGGATGGCGACCCGCGCGCCCATCCTCTGGCTCTCAACCCGAAAGCACT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCAGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGGCCCCATCAGCCCAACAA
GACCTTGCCTTTCATCTCCAACCGCGCGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCTTTCCCTTCGACATCAAGACCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTGCCTCTTCTGCGCTGGTGTGCTGTTTCTCTGAGCCGGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAAATGAAAGATGATATGAGGCGGGGCGGGGGCAGGGACCCCCG
GGCGGCGGGCAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCTTCCCACTC
CTCCCTACCCTTCTACACACGTTCTCTTTCTCCCTCCCGCTCGTCCCCTGCTGCCCCCG
CCAGCCTCACCACCTGCCCTCCTTCTTACAGGACCTCAGAAGCCGAGCCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAAACCGACGCGCGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTGAAATAATAAAAAAGAAAAAACTAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLELELNENIVSAVEPGAFFNNLFLNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLSNLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYLRLKVLEISH
WPYLDTMTFPNCCLYGLNLTSITHCNLTAVPYLA VRHLVYLRLFLNLSYNPISTIEGSMHLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVLNVSGNQLTITLEESVFHSGVGNLETLILDSNPLA
CDCRLLWVFRRRWRNLNFRNQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFDPDGTLEVRVYAQVQDNGTYL
CIAANAGGNDSPAHHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLFLWLSRGKGN TKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

[illegible]

CCACACGCTCCGCACTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCGGGGAAGCGCAATGGGGGCCCCAGCGCCTCGCTCCTGCTCTGCTCCTGC
TGTTTCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAAGTGAAAGATC
CGAGGACTCATCCCTGCAATGGTCTAACCTTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTTCAGCTGGTTACCTCTACGCCCCAGGAGTCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGTCTCAATCTTCACTATGCCTGT
GCGAAGTCCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCACTTCTTGGGAGCAAG
CCTGCAGCCGGCTCACTCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCACCCGCAT
ACAGGAAGATCCCAATGTTAAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGAGTAGTATGGGCGCAGCATCGTGTGCTGTGAACCATGAATCTTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACAACCACTAGCGGTATTAGGCCAGACC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGGTGCGCGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCCTGCCACTTCTCTGC
GCCCCCAGGGGGCCCTGTGGGGACTGCTGGGGCCGTCAACAAACCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCCGCTTGCTCCCAGCCACCCACCCCTGTACAGAATGTCCTGC
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGG
TGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC
CAATCAAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
ACAAAAAACA

FIGURE 32

MGAPAASLLLLLLFACCCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGKRALRDNRILVTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHCEGRGNPVPQQYLWEKEGSSVPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YVTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTAEAGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAACCCCTTTTCTTCTCCTTTCTCTGG
CTTCGGCAGATTTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTGT
TTACTTTTGTGATGAGATCGGGGATGAATTGCTTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCCTCTTTGTTTTGCGCGTGGAAACGTTACAGGGGACGTTTGC AAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACAGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCGCCCGACTTCCCGATTTTACCATTATTTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCAATGG
AAAACAATGGCTTGCATGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAGG
CTGCACATCAACAACAACAAGATCAAGTCTTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAATTTATACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACATCTCATCAGACCCTTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTTGGAGCAATCCCTGGTATTGCGGAGATCTGTCTAGAGGATAACCCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATTC CCAAGAATGCC
CTGATCGGCCGAGTGTCTGCGAAGCCCCCACCAGACTCGAGGTTAAAGACCTCAATGAAAC
CACCGAACAGGACTTTGTCTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCTGT
CCCAGAAGAGACCTTTGCTCTCTGGACCCCTGCCAACTCCTTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCTTAGCTTAACA
GTTTACCCTGCCCTGGGGCTGCAGCTGCGACCACATCCAGGGTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACCTGAGCAGCTTGCTGATTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAAATCGCACTTTGTGGATTACAAGA
ACCTCATCTGTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACCAACACTTTCAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTA CCTGGACACGCTGTCCCGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCTCTCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTCTATGTACCTCCCGTGGCAGGGGTGCTGGAACGACTTAACCTCCATCATCCAGA
TAGACCTCCACGGAACCCCTGGGAGTGCTCTCGCACAAATGTGCTCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCGGTGAACTTCTT
TAGAAAGGATTTTCATGCTCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACCTC
AACTCCTACCTAGACACACAGCAGGGGTGCCATCTCGGTGTTGGTCCCGGAGCTGCTGCTGGT
GTTTGTCACTCCGCTCTCACCGTGGTGGGCATGCTCGTGTTTATCTGAGGAACCGGAAAGC
GGTCCAAGAGACGAGATGCAAACTCCTCGCGCTCCGAGATTAATTCCTACAGACAGCTGTG
GACTCTTCTACTTGGCACAATGGGCCTTACAACGCGAGTGGGGCCCCACAGAGTGTATGACTG
TGCTCTCACTCGCTCTCAGACTTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGC
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAATACTGTGAGCTCGCAACAACCGAAAGGGCCT
GACCCCTTACTTACTGCTCCTCTTGAACAAGAGCAGACTCTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTCTGCTGAGAGCCCTTTTGACAGAAAGCCAGCAGACCCCTGCTGGAAG
AAGTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCTGTGGCTACGAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLRLRIDPGAQDLNKLVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIABILLDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLO
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNQGEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHIPGSGLKMNCNNRNVSLLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY
LDTLSREKFAGLQNLLEYLNVYNAIQLLPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNFYMYLPVAGVLDQLTSIIQIDLHGNPWECSCSTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPOLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSI SVL
VPGLLLVFVTSFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGTGACCCAGAACTACTCAGGGC
TGCACCGGGCTGGCAGCGCTCCGCACACATTTCTGTGCGCGCCTAAGGGAACTGTTTGGC
CGCTGGGCCCCGGGGGGATTCTTGGCAGTTGGGGGTCCTCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGTTTGGGGAAGCCAGCTGTAGAGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCTGCGGGCCCTCAG
AGAATGAGGCGCGGCTTCGCCCTGTGCCCTCCTCTGGCAGGCGCTCTGGCCCGGGCCGGCGG
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGCGGCCGAGGAGGCTGCATCCTGCGAGGTGGGCGGCTC
AGCACCGTGCCTGCGGGCCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCGSGAGGGGGCTCCAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCCTGCGCCGCGCCCCGGG
GCCGCCCTTAACCTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTTAACCTGACCTAGACGACTTGGGAGG
CTTTGCCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCGGCCACT
GCAACGAGCCCCGTGCCGACAGAAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCTCTGAACAAGACAATTGAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCAGGATGTCTACCCCTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCGAAGTTAATTCTACGACTTCCCTGCGCACTCCTCAGGCTTT
CGACTCCTCCTGCGCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCCCTCTTCCAGGCCA
AGGAAGGAGTCTATGGGCCCCCGGGCCTGGAGAGTGATCCTGAGCCCGTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCCGGGACTGTGATCTGCGGGACAGAG
CAGAGGTTGCCCTGCTGGCGGAGTCCCTCTTGGCTCTAGTGATGCA**TAGG**GAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACTTAC
TTGTGTAACGTACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCTTTAGGA
TGGTGTAACCTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTCTTTATGTTTATTCGGAGAA
TTTGGAGAAAGTGAATTGAACCTTTCAAGACATTGGAAACAAATAGAACACAAATAAATTACA
TTAAAAATAAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAAGGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGGAAAAATAAAAAATAAAAAATTAAAGGATGTTTGAT

FIGURE 36

MRPAPALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAEILRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDRSCVTSSEGOPTLGGTVGPTRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILMTMTVLGLVKLCFHESPPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCGCCGCCGCGGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGGA
GGGGCGTGTGTGCCGGCGCGCGCCGTGGGGTGCAAAACCCCGAGCGTCTACGCTGCC**ATGA**
GGGGCGGCAACGCGCTGGGCGCCACTCTGCCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCCTCCAAATAGCAAATGTACTTGGAAAAATCA
CAGTTCCCGAAGGAAAAAGTAGTCGTTCTCAATTTCCGATTATAGACCTCGAGAGTGAACAAC
CTGTGCCGTATGACTTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAAAC
CCCCAACTGGCCAGACCGGGATTAACCTGCAGGAGTCACCTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTAGGCCAAAA
AAACTGCCACAACTACAGAACAGCCTGTCAACCAACCAATTCCCTGTAAACCGGGTTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAAACATCACTCGCATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCTCAGAAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCCAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCCTTAAAAAATAAGCAATG
TTAA**CAGT**GAACGTGTGCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT
TCTCAGTAGAAAAAAAATACCTATAAAAATACATATTCTGAAAGAGGATTCGAAAGATGG
GACTGGTTGACTCTTCAATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCGTGCTGTCAAGGAGCAGCTATCTGATTGGAAACCTGCCGACTAGTGCAGTGTATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTATAGT
GTTATTTGTTTTCACTTCAAGCCTTTGCCCTGAGGTGTACAACTCTGTCTTGCCTTTCTA
AATCAATGCTTAATAAAATATTTTAAAGGAAAAAAAAAAAA

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG

FIGURE 38

MRGANAWAPLCLLLAATQLSRQQSPERPVFTCGGILTGESGFISSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPPTTEQPVTTFPVTTLGLKPTVALCQQKCRRTGTLEG
YCSSDFVLAGTVITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVCKQCPLLR
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGGCTGGGGCGGTTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTACATCTG
CCGGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTGGAG
GTGGAACACTGCCTGGGAGGAAGAAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGAGGGCCAGGTGCTGTGAAGAAGTGTAGCCCTGGCTATCA
GCAGSTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGGAGAGA
ACAAGCAGTGTGAAAACAACGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGACAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCC
TCCTGTCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTACCAACATCCCCACACCCCATTGCCACTTATTTATCTCATCTCAGGAAATAAGA
AAGGTCTTGGAAGTTAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCCSDSLKCCPAGTFGPSCLPCPGGTERPCGGYGQCCEGEGTRGGSGHCDQCAG
YGGEACGQCGLGYFEARNASHLVCSACFGPCARCSGPESNCLCKCKGWALHHLKCVDDIDE
CGTEGANCGADQFCVNTGEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGCGTGTGGAGGCCAGCACACCTGCTGGTGTTCGG
CATGGAGCAGCGGTGCCGCCCAACAGCGAGCTGGTGACAGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCCTGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGAATATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGAGGCCCTGGCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACATATTTCTAAGCACTTACAT
GTGGAGATACTGTAACTTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTGTGCAC
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAACATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLWCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGFLASGAHKLVRFASQGAPAGLGEPQLELHTLDDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASCSDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTCTCTCCCGGTGTGGAGTGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATAACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTTCATCGTGGCAGCCGTCTTGTAAACCTGATTCCTCTGGGAAT
CTTGTTTTTTGGCATCTGGTTTTGCCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTCTGGTGTGAGCCCTGGTCGGCTCACCGCCTATCATCTGCATTTCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCTGTAGTTTACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTCTCCTACCACTGCTGAGTGGCCTGGAACCTGTTTTAA
GTGTTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTCGCGGAATCTGCATCAACTGCCCACTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCCTGGCTCTTTCCTTGTTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATTGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTGAAGCCAAAAG
GATTTAAAACCGTGTCTCTAAAGAAAAAGAACTGGAGGCTGGGCGCAGTGGCTCAGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACTGAGGTGGGAGTTTCGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAATAACAAAGTTAGCCAGGCATGGTGGTGATGCCTGTAGTC
CCAGCTGCTCAGGAGCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYS GFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVIFLPTGITFKSVTREDTGTYYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCCTCGGACTAGGCCT
GGAGGCCGCCCGAGAGCCCGCTTTCACCCGACCTCTGCCCAGGCCCGCAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAAGTGCTTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGACGCGATGGCAGCGATGAGGAGGAGTGACAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAAGTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCTGGAGAGTGTCACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCTCTCTGTCGGGAATGCCACATCCTC
CTCTGCCGGAGACCAAGTCTGGAAGCCCAACTGCCTATGGGGTTATGTCAGCTGCTGCGGTG
TCAGTGCAAGCCTGGTCAACGCCACCCTCCTCCTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGCCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGCGCCCTGGAGATTGAGGGTCCC
TGGAACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGELRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTLRLNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGCGGAGGAGGGAAGGAAGCTGCATGTCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTCTACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTAATGGAACCTTAGGCTGGATCCCAAGTGA
TAATCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCTATGAAGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGCATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCGCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCAGCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT
GCCACCCGCGCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCCTGA
CCACGTGGAAGATTGTGGCGTTACACGGCAACCAAGTGTGCTGTGTTGCTGCTGCTGCTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATGCCCCACTGGGT
GTTGTTCTTAAGAAATGATTGATTAATAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTTCCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATGTCTATGCTGATAGAGTGGTGAGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAATAAATTAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQSPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPSSSSDPDFVVVD
GVPVMLPSYDEAVSGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDDTDGPGSESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHVWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTTCGGTGGCCTAGAGA
TGCTGCTGCGCGGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCGGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGGTGAACATGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCTTCTCCTCCTCCTTGTGGTACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAAAGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC
TGCCCTCTCCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCACGACCTCCTGTTGGACCCACGTTTTGGCTGTATCCTTTAT
CCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACTCTGTTTTCTTGTCTATACAG
CAGCATATTTATCATACAGACAGAAAATCCAGAATCTTTCAAAGCCACATATGGTAGCAG
GTTGGCTGTGATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAGAA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGD FWI GLRRREEKQSNSTACQDL
YAWTDGSI SQFRN WYVDEPSCGSEVCVVMYHQPSAPAGIGGPFYMQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREALNLAYILIPSIPLLLLLV
VTTVVCWVWICKRKRREQDPSTKKQHTIWSPHQGNSPDLEVYNVIRKQSEADLAETRDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSES GSFVTLVSVESG FVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCCGCGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAAGTGGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCAAGCTATTAGAGGTCCCACCCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTTCTCCTTACGACTCT
CAATACCATGAGACCCTGAAGGGGGCATGTTTGTCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCAGAGAGGTCTTTATTCTGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGTCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGATACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGTCTTAATGACCCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGGCT
GTTGACCTGACCATGGAACCTTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGACGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCACTTTATACCTTAAGCCCAGAAAAATACCATGCACCTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCTTTATACAATG

FIGURE 52

MITGVFSMRLWTFVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLCLKMKVQVVRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPITIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKR FARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-55

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCTTGGTCAATGGCTCTGCTATTTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGTCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGTCTCTATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTTCATGATGAAGATGCTGGGGCATCGTGTGAGAAGCCAGAGAGCTCTTTCTCCCCA
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGTCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG
TGTGCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGTCTAGTCTCAGGACGAGAAGCAACCCCTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAAGTGGGAGAAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCAGAGATTTTGGGGGTTTACGACTGCACCCACCAGGAAGA
TGTTGGCTGTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCATATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATATA
CACCATTGTCTGTCTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAAGGATAAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACCTTTATTTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPEAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEEDAGASC
ENPESSFSFVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSSCSGREATLQDCPSGFWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVMGVSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCCGCGGACGCGTGGGCGGACGCGTGGGCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTCGGGAATGTGTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCCTCCTTGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAAACACT
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGCGCGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTATTATGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVL CGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAILQCFCGYVDIL
VNNAGISYRGTIMDTTVDVDRVMETNYFGPVALT KALLPSMIKRRQGHIVAIISSIQ GKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDDTT
AQGRSPVEVAQDVLAAVGGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTCTAA
GAGGAGAAAATAGTCAACGGCGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCGCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTTCCTCTGCAATGACGAAGAATAACCATGGCCATATTGTCAGTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA
TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTTAATTTCTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCTGAGCGTTT
CCTGGCAGTTTTAAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACAGATTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCCTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCCAA
AATTTGTACCATAACCGTTTATTAAACATATATTTTATTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 58

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKS
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEENVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGVGFHKTLLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNL
MH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAVIGYKMKQA

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGTTCGACTAGTTCTAGATCGCGAGCGGCGCGCGCGGCTC
 AGGGAGGAGCACCGACTGCCGCCGACCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
 TTTCGCTGGTCTGTGATGCCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
 GTTTCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTTGAAGC
 TGGGAAGATCCAAAAAGGAAGAAATTGAGTTTGGTTCGGCCCTTTCCAGGACTGAACATGA
 AGAGTTATGCCGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
 TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
 AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTACAAAGTAACATGA
 CCTTGGCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATGTACAATCCA
 GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
 AGCACGGGATTTATACAGTGCACATAATTCAGTTTTTCCAGATATTTCTGAAATATAAAAAATA
 ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
 ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
 TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAAATTGGCT
 TGTGTGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
 AGGAAGCAGAACTGGTTTGGAGCCTTTGAATACTGGATAAACTACTAGATGGCGACTTAAC
 AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAAATTTTGGCGGT
 GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTGTCACTCCAGAGGTGAGACAA
 GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAGTTTGAAGAGTACTTGGCGAGA
 AGATACAGTACAGTCAAGTTAAGCCATGGTTAACTGAATCATGAATAATTATAAGGTTCTGA
 TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGCAGAGCGCTCCTTGATGGGC
 ATGGACTGGAAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA
 ATCTGACAGTGAAGTGGCTGGTTACATCCGCAAGCGGGTGACTTCCATCAGGTAATTATTC
 GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
 TTCATTTATGGAAGGATGGGATCCTTATGTGGATTAACCTACCTTCCCAAAAGAGAACAT
 CAGAGGTTTTTCATGTGAAAGAAAAATCGTAAAAACAGAAAATGTCTAGGAATAAAAAAA
 TTATCTTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATATCCTTGAACAAGTGAGC
 TTTTGTTTTGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
 TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
 AATTTTAGGGTCTTGAATAGGAAGTTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAAGTTG
 TAACAACAAAGCTGTAACTCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
 GTTTGGAATAATATTATGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
 TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
 AAAATATTATATATAAAGTAAAAAATA

0990766-071204

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGSGQPLFLTPYIEAGKIQKGRELSL
VGPPFGLNMKSYAGFLTVNKTYNSNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLSNPFVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLRREDTVQSVKPWLT
EIMNNYKVLINYGQLDIIVAAALTELSIMGMDWKGSGQYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAPDMINRFIYGKGWDPPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
TTTTCCCTTTCTCAACAAGTTCTAACAGCTGTTCTAACAGCTAGTATCAGGGGTCTTCTCT
GCTGGAGAAGAAAGGCTGAGGGCAGAGCAGGGCACTCTACCTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGGCTGCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAAACAGGATTCCCTGAAATTTCTTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAATGCAGAAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCTGGGTC
AGGCCAGCCTCTTTGTCTCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACAGAGAGCCGTCT
CCTCACCCCGCCCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCCTTGACCGT
CCACCAAGGGACGGGGGCGGTCTATGTGGGGGCCATCAACCGGGTGTATAGGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAGACAGGGCCAGAAAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCCTGCTGCTGGCTGTGGGAGCCTTACACAGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCTATCTGGTGGAGCCATCCCAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCTACGGCAGCGCTGTGGATGGGAAGCAGGATTACTTCCGAGCCCTGTCCA
GCCGAAGCTGCCCGAGACCCTGAGTCTCTCAGCCATGCTCGACTGCGCATACACAGCAT
TTTGTCTCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTTGACAT
CTTCTACATCTACGGCTTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCTGCAAGCTGCTTACTTGGCCAAAGCCTGGGACTCACTGGCCC
AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
CAGTATCACACCCCGCCGATGACTCTGCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCTGTCTACAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGCTCCAGTGCACGAAGGCCTGTGCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCAC
CAGCAGGAGCCGATGACCTCTGTGGCCTCTACGTTTACAACGGCTACAGCGTGGTTTTTG
TGGGACTTAAGAGTGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACCTTCTCAGCAAAAGTCCCTCTTGAAGGTAGCTATTGGTGAGATTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGGTGAAGTGGGGAGGTAAGAAGGGGTTAAATTTTGTG
ACTTAGCTTCTAGCTACTTCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTAAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAAA

990476-071001

FIGURE 62

MGTLGQASLFAPPNGNYFWS DHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQFWP
RALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSEN RDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLT MNVNKLLIIDYSENRL LACGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVD GKQDY
FPTLSSRKLP RPDESSAMLDYELHSD FVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLF AIFSKGQKQYHHPDDSALCAFPTRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLLKVRVYEFRCSNAIHL LSKESLLEGSYWWRFNRYRLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 64

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDMSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPDWLLQDPGMRLRTTYKGFTAEVDLYFDHLMSRVVPLQ
YKRGGP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLENVQGTQPKMVMMEYWTGWFDSWGPHNILDSSSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYIILYE
TSITSSGILSGHVHDRGQVFVNTVSI GFLDYKTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXSLEPETPLPAFFLGSL SIS
STPCDTFLKLEGWEKGVV FINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGTAGAGTGTAGGGGTGGACGGGTCCAGGACCT
CTGGTGAAGGGTCTCTACTTGTGGCTTTCGGTGGGGGTCAAGACGCGACCTACCGCAAAGG
GTAGCAAAGCGGGGCTCGGCCGAGGCCCCAGGACCTCCATCTCCCAATGTGGAGGAATC
CGACACGTGACGGTCTGTCCGGCCTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCTGCTCTCGTTCCTGCTGCTGCGCTCAGCTGACGCTACTGTGCCCCA
GGCAGACACTCGGTGCTTGTAGTGTAGTAGGGGTATGACCGGTTTCTCTAGCGGGGCC
CGTTCGCTGTATGTGTGTGGCAGCTGCACATTTTCGGGTACCGCGGGTGCTTTGGGCGCAC
CGGCTTTTGAAGATGCGATGGAGCGGCTCAACGCCATACAGTTTATGTGCTTCCGTGGAATCA
CCACAGGCCACAGCCTGGGGTCTATAAATTAAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCGAGCTTAGCGCAACCTGTTGGTCTACTTGAGCCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCTCGTGTGCTTCGAAAACTGAAATTCATCTAAGAACCTC
AGATCCAGACTCTCTTGCCGACGTGGACTCTGTTTCAAGGTCTTGCTGCCCAAGATATATC
TAGCTGCTTTATCAACCTGGGGGACATCATTAGACATTCAAGTGAGGAATGAATGTGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCATGCTAGG
AGAAAGATCTTGCTCTTACACCAAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCGGG
GACTCTATACCACTGTAGATTTTGGCCGAGCTGACAACTGACAAACAACTTACCTGCTCT
CGGAAGTGAATCCCATGGGCCATTTGGTAAACTCTGATGATACACAGGCTGGTGCGATT
CTGGGGCCAGAATCATCCACAGGCTGTGTGCTGAGTCAACAAAGCATGGAAGAACATGTC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGTGCGCGATGAAGAAGAGGACGCTTCTCTCGGATATACACGACTATGACATGATGCTG
TATATCTGAAGCAGGGGACCCACACTAAGCTTTTGTCTCTGATGATGTATCAGCAAGT
TCCAGGAAGTTCCTTTGGGACCTTACTGCTCCCCGAGGCCCAAGATGATGCTTGACACTGTG
ACTGTCAGCTGTGTGGGCATTCTAGCTTCTCTAGACTGCTTTGCCCCGTGGGCCAT
TCATTCAATCTTGCCAAATGACCTTTGAGGCTGTCAAGCAGGACGAGGCTTCATGTTGTACC
GAACCTATATGACCCATACATTTTGGAGCCAAACGACTTCTGGGTGGCCAAATATGAGGTCT
CATGACCGTGCTTATGTGATGTGGATGGGGGTCTCAAGGTTGTGGTGAGCGAAATATGAG
AGACAAACTATTTTGTAGCGGGAACTGGGGTCCAAACTGGAATCTTGTGTGGAGAACATGCG
GGAGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGCTCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCTCTACCCAGTGGATGATGTTCCCTCGAAAAATGTAAACCTTGTGAAGTG
GTGTTTTCCTCCAGTTGCCAAATGGCCATATCTTCAAGCTCTTCTGCCCCACCAACTTCT
ATGCAAAAACATTTCAAAATTTAGGCTCAGTTGGGGACACATTTCTATATCTACTGTAATG
ACCAAGGGCCAAAGTCTGGATCAATGAGTTTAACTGTGGCCGATGTGACCAAGCAGGGGCC
ACAACGACCCTCTACGTGCCAAGATCTCTGCTGTTTCTTAGGGGAGCCCTCAACAAAATCC
CATTGCTGGAACTAGAAGATGACTCTTCAGCGCCCAAGTCAATTTTGGATAAGCCTATC
CTCAATGACACTAGTACTTTGACAGGACACATATCAATTCCTTTCAGCTGATACACTGAG
TGCTCTGAACCAATGAGATTTAAGTGGGCATGGAAGGTAGGCGGGCAGTGTGGCTCATGCG
CTGTAATCCCGACACTTTGGGAGGCTGAGACGCGTGGATTACCTGAGGTCAAGACTTCAAGA
CCAGCCTGGCCAACTGGTGAAACCCCGTCTCCACTAAAAATACAAAAATAGCGGGCGGT
ATGTTGGGCACCTCTAATCCAGCTACTTTGGGAGGCTGAGGCGAGGAAATGCTTTGAATCC
AGAGGCGAGAGTTGTGAGTGAAGTGGAGGTTGTACCACTGCATCTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAATAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRS FVVD RGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRL LKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDLAAVD SWFKVLLPKIYPWLYHNGNIIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNM TKIF
TL LRKYEPHG PLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM YMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGLPPSPKMM L
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFFWVFN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWT KQG PQOTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTL SASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 47

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTtagTGACATTCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTTCACATGGTAGACCAGTATGACCAGCTATATTCGAAGCGTTTTGGTGTGTT
CTTGTGAGAAGTTAGTGAAAATAAACTTAGGAAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTCTTCGCGATCACTTGAGA
TGCCCTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCTGGGTGATTTGTCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTCCAGCATTTAAACGACT
GACTTGTTTAAAATTATGGCATAACAAAATGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTATTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCBAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGTCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAGTG
CTTGGACCGCCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTTGTATACCCTGCCACTCGAAGTCAAGAGGCATTGAATCAAGACATA
AATATTCCTTTGCAAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGTCTACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGTTTTTAAGTCATTCAATTCCAAATCATTTTTTTTTTTTCTTTGGGG
AAAGGGAAGGAAAAATATAATCACTAATCTTGGTCTTTTTTAAATTGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TCTTACTAAAAAAAAAAAAAAAA

FIGURE 68

MAYMLKLLISYISIIICVYGFCILYTLFWLFRIPLKEYSF EKVREESSFSDIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHFLMLSG
VPDAVFDLTDLDVLKLEL IPEAKIPAKISQMTNLQELHLC HCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNS ENNMIGLESRLREL RHLKILHVKS NLT KVPSN
ITDVAPHLTKLVIHNDG TKLLVLNSLKKMMNVAE LELQNC ELERIPHAIFSLSNLQELDLKS
NNI RTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRLCDVSYNNISMIP IEIGLLQNLQHLHITGNKVDILPKQLFKICKLR TLNLGQNCITSLP
EKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDH LFD TLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCGCGCCCTTCTCTGGACTTGGCATTTCATTCTCTTTTCATTGACAACTGACTTTTTTTTATTCTT
 TTTTTTCCATGCTCTGGGCCAGCTTGGGATCCTAGGCGGCCCTGGGAAGACATTGTGTGTTTTACACACATPAAGGAT
 CTGTGTTTTGGGGTTTTCTTCTCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTGGGAGGGGAGACCACCTGG
 GCTCAGTGCTTGTCTGACCTTATCTGCTAGGTACATCGAAGTCTTTTGACCTGCATCAGTGATTGCTGCTGTC
 ATCGCTGGTGGTATCCTGGCGGCCCTTGCTCCTGCTGATAGTGTGCTGCTCTGCTCTTTATCTCAAATAACACCAAG
 CGCTAAAAGCTGCAAAAGAACCTGAAAGCTGTGGCTGTAAAAAAATCACAAACCAGACAGGCTGTGGTGGGCCAAG
 AACAGCCAGGCCCAAACCATTTGCCACGGAGTCTTGCTCCTGCCCTGCAGTGCTGTGAAGGATATAGAAATGTGTGGC
 AGTTTTGATTCCCTGCCACCTTGGCTGTGCGACATAAATGAGGGCTCTGAGTAGGAAAGGCTCCCTTCTCAA
 GACAGGCCCTGGAAGACTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
 CTCCCATCAGTTTCTATGGAAAAATACTCAGTGCTGCTGGGAACCAAGCTGTGAGGATCCCTACAGAGAGCTTC
 CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGGGAATGCTGATAAACCCAGTCA
 CACAGCTGCTTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAAGTACGCTTCCCTGGAGGTGTCCAGAAA
 GCTGATGTAAACAGAGCCTATAAAAGCTGTGGTCCCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
 AGAAGGCTCATGCCATTGACCCTCTTAATCTCTCTCTTGTGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCACTAGGGGGTGCCAAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
 AGTGAGAACTGCACCTGGACAAATAGAAAGACCAAGAAAAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAAGTGAAACATTAAAGTCTTTGACGGAACTCCAGCAATGGGGCTCTGCTAGGG
 CAAGTCTGCAGTAAAAACGACTATGTTCTCTGATTGTAATCATCATCCAGTACATTGACGCTTCAAATAGTTACT
 GACTCAGCAAGAAITCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTTAAGATCTCTATTCCAAACTGT
 GCGGTATACCTGGATACCTTGGAAAGGATCCTTCAACAGCCCCAATTACCCAAAGCGCATCTGAGCTGGCTTAT
 TGTGTGTGGCACATACAAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTCCTAGAAATAGAC
 AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGGCTGATTGGAACAAGCTGTG
 GGCGGTGTGACTCCCACTTCGAATCGTCATCAAACTCTCTGACTGTCGTGTGTGTACAGATTATGCAATTTCT
 TACCGGGGATTTCTGCTTCTACACCTCAATTTATGCAGAAAAACATCAACACTACATCTTAACTTGCTCTTCT
 GACAGGATGAGAGTTATTATAAGCAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCACACTAAAA
 GACCCAACTTGCAGACCAAATATTCAAATGTTGTGGAATTTCTGTCCCTCTTAATGGATGTGGTACAAATCAGA
 AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACTTTCTGCACTCTCAACTTCTGGAAGTATCACC
 CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATCTCAGTGGAGATATAATACATAACA
 GAAGATGATGTAATACAAAGTCAAATGCCTGGGCAATATAACACAGCATGGCTCTTTTGAATCCAATTTCA
 TTTGAAAGACTATACTTGAATCACCATATTATGTGGATTGGAAGCCTTCTTTGTTCAAGTTAGTCTGCAC
 ACCTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTTCCCACTCTGATCTTGGATCTCCAACT
 TACGACCTAATCAAGAGTGGATGTAGTGGAGATGAAACTGTGAAGGTGATCCCTTATTTGGACACTATGGGAGA
 TTCCAGTTTATAGCTTTAAATCTTGAAGATGTAGCTCTGTGATCTGCAGTGTAAAGTTTGTATATGTGAT
 AGCAGTGACCACCACTCTGCTGCAATCAAGGTTGTGTCTCAGAAAGCAACGAGACATTTCTCATATAAAATGG
 AAAACAGATTCCATCATAGGACCAATCTGCTGAAAGAGGATCGAACTCAAGTGGCAATTCAGGATTTCCAGCAT
 GAAACACATGCGGAGAACTCCAAACCAAGCTTTTCAACAGTGTGCACTGTGTTTCTCTCATGGTTCTAGCTCTG
 AATGTGGTGAAGTGTAGGCAACATCAGTGAAGCATTTTGAATCAACGGGAGAGCTACAAATACCAAGAGCTG
 CAGAACTATTAACCTAACAGGTCACACCTTAAGTGAAGCATGTTTCTCAGGATGCCAAAGGAATGCTACCTCGT
 GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACAGGCCCTGCATGTAAAAAA

FIGURE 70

MELVRRRLMPLTLILLISCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGGSCSENIKVPDGTSSNGPLLGQVCSKNDYVPVFESSSSLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSTSPNYPKHPPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQQLQIIVKCEMGHNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPPYYVDLNLQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLI CDSSDHQSCRNCQCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFGHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATTIVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTTCGCCGTTCGCTGCTGTTGCTGTTGCTGC
TGCTGCCGCCGCGCGGTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGCGGAGTCC
CTGGACGCCCCGACGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAAATATGAAGAT
TTTGGACCACTATTTACAGCAAATTTTTTAATGCCAACCATGTTGGGCAGATATTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTTACCCTTGTGGGGGT
CAGAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTGGACTGTACTATTCCTTTTGA
ATGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGTTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGTTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACGTCATGACAATAGACAACTGTCTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGCCCACTAGATGGCACCATTTCGTAGTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTTGCTAAAAGTCAATGGAGAGCTATTTATGAACCTA
TACCTGGCGATCCAGAATTGACACTGTACCCCGAGATGTGTGGTACACATCCAAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT
CCCAAAGCTATTCGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTTATGGTGAAGCTGCCACAGTAAACCATCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAATTTATTTGGCAGTTCAGCCCTTTCCTTTTTTCCCACTA
AATTTTTCTTAAATTACCATGTAAACATTTTAACTCCTCAGTGCACTTGGCCATTAAAGTC
TCCTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCACTATATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGTCTAGTCAAT
TTTTTTTTTGTGCCAACATCATAGAGTGATTTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGCTATATCGAAACATATGGAACATAGAGAAG
GTACAGTAAAAATAGTGTAAAATAAATGGTGACCTGTATAGGGCACTTACCAGCAATGGAG
CTTACAGAGCTGGAAGTTGCTCGGGTGAGTCAGTGAGTGAATGGAAGCCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAA
GTTTCTTTCTTCTTCAATTATAAATAAATAAGTGTACTGTAAACGTTTAACTTTTAAAT
TTTAAACCTTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAACATAAATCATTTGTGCAA
ATGTAA

CGGCTGCGCGGCTGCGCCG

FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPGSEWFWWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAINRNTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESFPVRGTVVINDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTTGCCTGCAGAAGAGCT
TTCCATCCAGGTGTCTGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCCAGC
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTGCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTTCAACTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCAACCAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAAATTTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCCT
ACTCTACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTTGATTGTGTACAGAAGTTTATTGGAACCTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTC
CCACGGCTCTGCTAGTGTCTGTCTCTCTCTCTCTTCTTGGTGTCTGCAGCTGGTCTTGGATTGTG
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGACTCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA
AACTGATAAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCTGGAA
GCTGAAGTTTACATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCTGCCCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCCTT
GGTTCCTAACTGGAATCAGCTCAGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAATGC
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCTACCTCCAAAGCTTCCACGGCC
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGAGTTTTCGAAAGTGCAA
GGACCTAAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCGCGAGCTCAGAC
CCTTTCTTCAGCTCTGAAAGAGAAAAACGCTATCCCACTGACATGTCCTTCTGAGCCCGTA
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGA
ACCTAATCTCTGTAAGACTAAAAATAAGAAATAGAACCAAGGCTGAGGATACGACAGTACACT
GTCAAGCAGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTCTGAACACATTGAGTTGGA
ATCACTGTTTGAACACACACACTTACTTTTTCTGGTCTCTACCCTGCTGATATTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAACTCTTATAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATCA
ACAAACATTTGTGAATAGCTACTATATGTCAAGTGTCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAAATTGACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTGTTGCTGAGACTAATCTT
ATTCTATTTCTCTAATATGGCAACATTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTTGTAACCTCTATATACCAAGCAATTTTAAAGTGCCATTACAAATGTATCACTA
GCCCTCCTTTTTCCAACAAGAGGACTGAGAGATGCAGAAATATTTGTGACAAAAATTA
AGCATTTAGAAAACTT

Figure 73

FIGURE 74

MARCFSLVLLLLTSIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTBAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGCGGCTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTC
TGATGACGTGCAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAT
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAAATGTGATCCGAGAAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGA AAAA CAAGAAGGATAAA **TAA** GATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTINATTNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGCGAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCTTACAGGAAGGCCTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTTCATATTCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAAATTTTCCCCAAGGACTCTTGCTTCCCTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAGATATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTTGAAGACAATATTGAACAACCCCTATTTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGAGGAGAAATCCCTGGACTTTCAC
TAACCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPPYYLLSALLSAAFLLRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

[illegible][illegible]

FIGURE 78

MGLLLLVLPLLLPGSYGLPFYNGFFYYSNSANDQNLGNHGKDLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWKLSENGAPEKDLVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVPFYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGTCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGACACAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTTGACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACACAGCCC
CTGGTGGAAGCCAACCACTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGGAG
GCAGATGCAGTCCAGGCATCTCTGCCCCTGGGCTCTCAGGAGCCCCCTGGGTGCGCTTC
TGTCCTGTGACACCCCAACCCAGGGAGGGGCTGTATAGTCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCTGCTGGCCTGGCCTGGGACACCTCTCTGTCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQ GKPSPDAGPHGQGRVHQAAPLS DAPHDDAHGNFYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDRGVRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD SMATRE
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEP AWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVWLPPAQDQPLVEANHLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGGAGCCCCGG
GCGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTCGCTCCAG
CCTGTCTGTGCTGTTTGGCGCCCCCGCTCCCGCGGGTGCGGGGTGCACACCGATCCCTG
GGCTTCGCTCGATTTCGCCGCGAGGCGCTCCAGACCTAGAGGGGCGCTGGCTGGAGCAG
CGGGTCGTCTGTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACGCGCGGGGCTCCGCAACCTGGCCTTGCCGCACTTCTCCCTCTCTCCAG
GTGTGAGCAGCCTTATCAGTCACTATGTCCGAGCCTGGATCCCGCTCTCGGCCTCGGTGTG
TGTCTGCTGTGCTGCGGGGCGCCGCGGCAGCGAGGAGCCGCTCCATTGCTATCAGTATG
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTCACAGTAACATAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCGAGAAAGAAAACCTGG
CAATAAAGATGTAAAGCAGACATTGCAATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTTACAGAAGAATTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCACATGTGGGCCTTGTTCAGGCCAGTGAACATCCAAAAATAGAATTTTACTTGAA
AAACTTTACATCAGCCAAAGATGTTTTGTGTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCCAATACAGGAAAAGCCTTGAGCATACTGCTCAGAAATCTTTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTACAGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
AAGAGAATGTCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTTCCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTTGTACAGATGGGCAGTCCATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCGAGGAATCACTATCTTCTCTGTGTTGGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCAGCCTTCTTCAAGAGAGTTCACAGGATT
AGAACCAATTGTTTCTGATGTCATCAGAGGCATTGTAGAGATTCTTAGAATCCCAGCAAT
AATGGTAACATTTTGACAACTGAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTTGTATT
CTCATAAATCTGAAATGCTTTAGCATACTAGAATCAGATACAAAACATTAAGTATGTCAAC
AGCCATTTAGGCAAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAAATTTACAGTGT
ACTTTGTTAAAAAACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAAACCTTTAAGAGTTCTAACCATGCCACTAGATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAACTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLLPGPAGSEGAAPAIATCTFTRGLDIRKEKADVLCPPGGCPLEEFVSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSSTQEBATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLC THEQMMCSKTCYNSVNIAPLI
DGSSSVGDSNFRMLLEFVSNIATFEISDIGAKIAAVQFTYDQRTFSTFDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRES PNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEAAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCACAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

Case	Age	Sex	Site	Pathologic Findings	Survival
1	65	M	Rectum	Adenocarcinoma	10 mo
2	68	F	Rectum	Adenocarcinoma	12 mo
3	72	M	Rectum	Adenocarcinoma	18 mo
4	75	F	Rectum	Adenocarcinoma	24 mo
5	78	M	Rectum	Adenocarcinoma	30 mo
6	80	F	Rectum	Adenocarcinoma	36 mo
7	82	M	Rectum	Adenocarcinoma	42 mo
8	85	F	Rectum	Adenocarcinoma	48 mo
9	88	M	Rectum	Adenocarcinoma	54 mo
10	90	F	Rectum	Adenocarcinoma	60 mo

AAAA

FIGURE 86

MRLLVAPLLLAUVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVCNDLFLTA
VPPALPAGTQTLLQLQNSIVRVDQSELGYLANLTEDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAIILDMNFRPLANLRSVLGAMNLRREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSDKFFALVNL
ELTKLDITNPNRSLFSIHPRAFHHLPMQETMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFTIEPQSTLCAEPPDLQRLFPVREVPFREMTDHCLPLISPRSFPPLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVVPEGTLELRRVTAEAGLYT
CVAQNLVGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPYHILLSSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIATILALAVLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSRRV
SAPLVLPWNPRKRLPRSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

[illegible]

CACAGCCACGGCGCTGTTTGGAGAAGGTGAAGAAGTTCTCGACCCTATGTGGAGGAGGGGGACATTTGTGTACCGCCT
 CTACATCGCGCAGACATCATCAAGCTGACAGGTGACATCTCATCATCTGTCACACCGCTCTACTACGTGACACAA
 CATCAAGTTCCACGCTGGAGCTCAAGCTGGACATTTAGAGGATCTCAGGGCTACCGCAGCTACCGCTGTGCCACC
 CTTGGCCACATCTTTCAAGATCTTCGGCTCTTCTATCATCGAGCTAGTACATCTTTCAGCGCTCATCTGATGTGTA
 CACATCTGGTGTGGTGTGCTACGGCGTCCCTCAGAAGTACTCGTTTGTAGTGCATCTCGTGAGGAGAGAGCTACGAC
 CGACATCCGCCGAGCTCAAGAACGACATTCGCTCTTCTGTCGACCTCATTTGACCAATACACCGCGCTCTACTGTCAA
 GCGCTTCGCGGCTTCTTCCTGTGCGAGGTGAGTGAGAACAGCTCGGCCGACGAACTTCAACAAACGAGTGGACGCT
 GGAACAAGCTTCGGGACGGGCTCACCACGAAGCGCGAGGACAGCTGGAGCTGCACCTCTTGTTCATGCTCAGTGCGA
 CCTGTACAGTGTGTTTGACTGTGGAGCTGGAGGTTCTCAAGTGGAGGCTACCTCCGCGAGTGACCATCCGCGC
 CAGCATTTGCCAGCTCACGGGCTCAAGGAGTGTGGCTTATACACACAGCGGCCAGAGTTGAAGCGGCTTCGCT
 GGGCTTCTGTGCGAGAACTCGGGCGGCTGCATCAATAGTTTACCGACATCAGGAGATCCCGCTGTGGTATCTA
 TAGCCTTGAGAACACTGAGGAGAGCTGCACTTGAGGCGCAACTGAGCGGGGAGAACACCGCTACATGCTCATGCA
 CGGGCTCGGGAGCTCAAAAGCCTCAAGGTGCTGGGCTCAGAAGAACTTAAGCAAGCTGCCACAGGTGGTGTCA
 AGATGTGGGCGTGCACTGTCAGAAAGCTGTCATCAACAATGAGGGCACCAAGCTCATCTGCTCTCAACAGCGCTCAA
 GAAGATGGCGAACTCTGACTGAGCTGGAGTGTATCGGCTGCAGCTGGAGCGCATCCCCATCTCATTTTCAGCT
 CCACAACTTGCAGGAGATGAGCTCAAGGACCAACCACTCAAGAACCTGAGGAGATCATCGCTTTCAGCAAGCT
 GACCGCGCTCACTGCTTAACTGTGGTGAACAACCATGCGCTCATCCCATCCAGTCCAGATCGCGAACTCACAA
 CTTGGAGGCGGCTTCTACTGAAACCGCAACAAGATCAGAAGATCCCCACCGACTCTTCTACTGTCGCGAAGCTCGG
 CTACTTGGACTCTGAGCAACAACTGACACTTCTCTTCGCGCAATCGGCTCTTCTGAGAACTCTCAGAACTCTCAGAACT
 AGGCTACCTGCGGCACGAGTGAAGACGCTCTTCGCGAGCTCTTCCAGTTCGCGGAAGCTCGGGGCTCTGCACT
 GGGCAACAACGTGTCTGAGCTCACTGCCCTCAGGGTGGGCGAGCTGACCAAGCTGACCGAGATCGAGTGTGTCGGGG
 CACCGGCTGAGTGCTGCTTGTGGACTGGGCAAGTCCCACTGCTCAAGCGCGCGGCTGTGGTGTGGAGGG
 GGACCTGTTCAACACATGCCCTCCGAGGCTGAAGGAGCGGCTGTGGAGGGCTTGACAAGGAGAGCGCT**TGAG**CGGAG
 ACGCGCCGACACAGCAAGCAGCAGGACCGCTCGGCTGACTCTCAGGCGCGAGGCGGAGCGCTAGCTTCTCCGAG
 AACTCCGAGCAGCGAGGACAGCTCGCGGCTGGGCGAGGACCTGGGGCGGCTGTGAGATGAGGCGAGGCGAGGA
 GACAGATATCTGTGGGGCTGAGCCTTTCTTCCCTTGAGACTGACCTCCCGAGGCAAGTGTCTGTGAGAGAG
 ATCCAGCTCAAGAGCTCGGATATTTGGATATCAGGTTCTCTCTCTGAGGCGAGCTCTCCGAGGCGAGCTCTGCGGAGGCTGAG
 CTGCACTCAGGAGGCTCTGGAGATTTGCATTTAGTCTTTGTTTATTTTATTTTCCATCTCCCACTCTCTTCACT
 AGATAAGTTTATACATCTCCAGAAAGTTTCAGGCCAGATGGAAGTGTTCAGGGAAGGTGGGCTGCTTTTCCCT
 TTGTCCTATTTTAGCGATGCGCGCGGCTATTAAACCCACTGGACTTCAGCAGAGTGTCTCGGGGCGAACAGC
 CAACTGGGACGGTCCACCGACGATGCGCGGCTGGGCTCTGCGGTGCGCTCCACGGGAGGAGCAGGCGCTCCAGCTGGG
 AAGGCGAGGCTGGAGCTTGCTCTCAGTTTGTGCGAGTTTAGTTTTTGTTTTTTTTATTAACAA
 AAACACTTTTTTTTTTAAAAAAAGTTTGAAAAATGAGATGTGTGGGTTATAAAGAAAAAATAAAATTA
 AAAGACTCAACGGCGAGTGAAGTGTGAGCTCAGGCGAGGTTGGGATTTCCCTTGAGCAAGACGAGCAGAGCT
 TGAATCTGTGTTCTTCTTCCTGGGCGAGGTTGAGGTTCTTCGAGATCTGGTGTGACCTTTGTCACAGGAT
 CTATTGTGCTTGGGAGGAGGTTTTTTTGTGTTTTTGGGTTTTTTGGTGTGTTTGTGCTTTCTTCTCTCTC
 ATGTGTTCTTGCGAGCACTATTCTGTGGCTGTGCGCGAGGAAATGTTCTGGAGTCTGCAAGGAGGAGGAG
 ACTCGGTTTGGCTAATCCCGATGAAGCGTGTCTCAITGCACTCCCTCTCTGTCGCTGCCCTGCTCTTCA
 CGCATGCTCTTGAAGGCGCCAGAGGAGCTCACTCGCCAGACTTTGTTTCCCACCTCTCGGGGACGGGTGTG
 CCAGTGCCACCGCTGCTCCGCTGCTCTCATCAGCGCTCTCGCCACTGTGCTCATGAGACGACACACTTA
 GAGGCTGTGTCGGAATGGGAGGCTCGCCCTGGGAGGAGCGGCTGTGGTTCAGAGCCGGTTCGGCTGCTCGGCT
 CTGGATGGTCAACGCGAGCTCGGCACCTGTTGGCTGGAAGCACTTGTATGACTCGGGTCCCACTCT
 AGAAGAGGCTCCCGCTTATGATCAATCAGTGTGACATGAAGCACTGTTAGAGTCTCTGTCTTAAGATTATGT
 CCATCGCTGTGCTGCTCAATTGTGTTTCTGCGTGTGATCATGTGATATCTCAGAAATAATGCACATAG
 CTTCTGACCAACCTGAAGACAAAATCGTTACATGTGGGCTGAACTGTGAGCTCGGTACAGATTCAAATAA
 ACTTTAAGACGAAAAAATAAATAA

FIGURE 88

MRQTIKVIKFILIIICYTVYYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFS LHN LQ EIDLKDN NLKTIEEIIISFQ
HLHRLTCLKLWNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDSLHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCTGAACGCAGGAGCTGTCTATTGACT
GGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCAC TGGATTTGGAAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACACGAAAACACCTGGCTCCAGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCATCGGGTTCAGTTATGTGAATGGTAGTGGTGCCATATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTGAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTTGGATCTCCCTGTTGATTGCGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACTTCTATAACATCTTAAC TAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTGACGCGC
CACGTGAGACACCTACAACGAGATGCCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGGTATATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG
GGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTGAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCCTAAATCTTTGGAACATCTGCTTTTGTCAAGTCTTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAA TAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPFVGTGFSY
VNGSGAYAKDLAMVASDMMVLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLWSGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETSFAVKS YKNLAFYWILKAGHMVP
SDQGDMA LKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGC'TTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGAGGCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCCTGCTTCGGTGACTCAGGTGGACCTT
GGCCTGTAAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTGCGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCCTTTGAGTGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGCTTCTCTTCTGTCTTGTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGEDAELGRWPWGSLRLW
DSHVCVGSLLSHRWALTAACFETYSDLSDPGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGAGCCGACACAGCGGAGGACGC
 TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCTGAGGAAGAGCTGAGTCTCACCTTT
 GCCCTGAGACAGCAGAAATGTGGAAGAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGATCCAG
 CTCTCCTCAATACGGAATACTGACCTAGAGAAATGTGGCTGATCTGGTGAGGGCCATCCC
 CACTGACCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAAGTGGCATTCT
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAGCAGAGCTGTGCTCTCC
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAGGTTCCAC
 ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
 TTTCCCCCAACATCATCCCTGAGGCAACGTCTTGAGCCCGAGGTGACAGGGACTGTAGGCCT
 GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATAACAATTGACCTCACAGACGTGG
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTTGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTCATGCGCCTCTTGGTGGCAACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACAACAGGCCGGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCACT
 ACCTGATGAGTGTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GCACAGGAGCCCTTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGTCA
 AACTGAGCTCATGAAGGCTGCCCTCGGGGTCTCACCTGTCTTTCGCTCAGGTGACAGT
 GGGGCCGGGTGTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
 CCCCTATGTACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCTCATCAAAATGAAA
 TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG
 GAAGCTGTAACGAAGTTCTTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGT
 CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTTCTGATGGCTACTGGGTGGTCAGCAACA
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTCTACTCCAGTGTGTTGGGGGGATCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCTCTTGGCTTTCTCAACCCAAG
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCCTGTC
 TGGATGAAGAGGTAGAGGGCCAGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC
 TGGGGAACACCAACTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCTTTCCCTATC
 AGGAGAGATGGCTTCTCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCCTCCTAACCCCTGAAA
 TGCTGTGAGCTTGACTTGAACCTTACCATGCTCCATCATATCAGGTCTCCCTACT
 CCTGCCCTAGATTCTCAATAAGATGCTGTAAGTACTGATTTTGAATGCCCTCTCCCTCCGC
 ATCTCATCTTCTCTTTTCAATCAGGCCTTTTCCAAAGGGTTGTATACAGACTCTGTGACTA
 TTTCACTTGATATTCATCCCCCAATTCACTGCAAGGAGACTCTACTGTACCCGTTTACTCT
 TTTCACTCCCTGACATCCAGAAACAATGGCTCCAGTGACATCTTCAACTCTTTCCTTTATGT
 GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTACTGCTCCAGGTCTTAACTTCTCTG
 ACTACTCTTGCTCTCTCTCTCATCAATTTCTGCTTCTTCAATGGAATGCTGACCTTCATGTC
 TCCATTTGTAGATTTTGTCTCTTCTCAGTTTACTCATTGTCTCCCTGGAACAAATCACTGACA
 TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATCACTCAAA
 TGTAAAAA

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FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYQKYLTLNVADLVRPSPLTLHTVQKLLAAGAQKCHSVITQDFTLCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDESLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGLFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPGWDFVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCGCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGTGCTCGGCGCGGAACAGTGCTCGGC**ATGG**CAGGGATTCCAGGGCTCCTCTTCTTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCTTGAAACCCACTTG
GCCTGCATACCGCTCCTGTGCTTGGCCCCAGTCTACCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGACCCAGTGTCTATAAGGGAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTTTTGGGAAGGACTTCTGTCTCAACTACCTTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCTGGTGGCAGAGAAGCATGTCTCACAGCTGCCCACTGCA
TACACGATGGAAAAACCTATGTGAAGGAACCCAGAAGCTTCGAGTGGGCTTCTTAAAGCCC
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA
ATTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCATTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTCAGG
GCACCACTGGGTGGACATGAATGGTTCCTCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCCAGATTGTCTATTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTTCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC
AAATGTTTTTTGTTCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGAAGGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACCTTTTCATAGAAATAA
AAAAAATCACTGATTTGGGGCAATGAGGAATATTGACAATTAAGTTAATCTTCAGTTTTTG
CAAACTTTGATTTTTATTTCATCTGAACCTGTTTTCAAAGATTTATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPFVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRTHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCCGCCCCACCAGGCCATGGTGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCTCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTACCAGCCGCTGGGTGATC
ACTGTGCCCACCTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCAGAAAGGTGGGTGTTGCCCTGGGTGGAGC
CCCACCTGTGTATTCTTGGAAGGAAGGTGCCCTGTGACAGCATTGCCCTGGTGCCTCTCGAG
CGCTCCATACAGTCTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC
CCCACCTCAGACCTGCGAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGATGCTTGTCTGGGCGACTCCGGGGGCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCCAACGGCCTCATGTCCCGCCCCAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTTGTAACCTGCCCCACATATCTTATTATTCTCCAATTTCAATAAATTATTAT
CTCAAAAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
M V V S G A P P A L G G G C L G T F T S L L L L A S T A I L N A A R I P V P P A C G K P Q Q L N R V V G G E D S T D S E W P
W I V S I Q K N G T H H C A G S L L T S R W V I T A A H C F K D N L N K P Y L F S V L L G A W Q L G N P G S R S Q K V G V A
W V E P H P V Y S W K E G A C A D I A L V R L E R S I Q F S E R V L P I C L P D A S I H L P P N T H C W I S G W G S I Q D G
V P L P H P Q T L Q K L K V P I I D S E V C S H L Y W R G A G Q G P I T E D M L C A G Y L E G E R D A C L G D S G G P L M C
Q V D G A W L L A G I I S W G E G C A E R N R P G V Y I S L S A H R S W V E K I V Q G V Q L R G R A Q G G G A L R A P S Q G
S G A A A R S
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAACCGGCCCTACAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGAAGATGCTCAGGATTTGCCTTACCTGGTAACAGAGGCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGTTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCATGTTCTATCCCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCATGCCCAGGAGGAGGCTGAGGCTGAGGTGCCTCCTTCCAGTG
AGGTCTTGCGCTCAGTTTTCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTGAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTCACTGTCTCTGTGTCATCTTCCCCACCCTGTCCCCAGCCCTAAACAAGATA
CTTCTTGTTAAGGCCCTCCGGAAGGGAAGGCTACGGGGCATGTGCCTCATCACCATATCC
ATCCTGGAGGCACAAGGCTGGCTGGCTGCGAGCTCAGGAGGCGCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCTTGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCTGAGTGCCTG
TGAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACTT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATGTPVGALTDEEKRLMVELHNLRYAQVSP TASDMLHMRWDEE
LAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSF RATEASDSRKMGT PSSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPFSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKFGELOATLDHTGHTSSKSLPNFNTSATANATGGRALALQSSSLPGAEGPDKPSV
SGLNSGPGHVWGPLLGLLLPFLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

0004756-071201

FIGURE 101

GTAACTGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAATTTCGGTCATTCTCCAAGTTAT**TATG**GTGGACGT
 ACTTCGTGTGTTCTCCCTCTGCCTTGCTTTTTCACATTAGCAGACCGGACTTAAGTCACACAGATTATCTTTTCAT
 CAAGGCAAGTTCATGAGCCACTTCAAAGCCTTCGAGAAGTGAAACTGAAACAACATGAATTGGAGACCAATCC
 AAATCTGGGACCACTCTCGGCAAAATATTACACTTCTCTCTTGGCTGGGAACAGGATTTGTTGAAATACCTCCCTGA
 ACATCTGAAAGAGTTTCACTGCCCTTGAACCTTTGGAGCTTAGCAGCAACAATATTTTCAGAGCTCCAAAATGCAATT
 TCCAGCCCTACAGCTCAAAATCTGTATCTTCAACAGCAACCGAGTCACATCAATGGAACTCGGGTATTTTGACAA
 TTTGGCCCAACACACTCTTGTGTTAAAGCTGAACAGGAAACCGAATCTCAGCTATCCACCCAAAGATTTTAAATCT
 GCCCAACTGCAACATCTCGAATTGAACCGAAACAGGATTAATAATGTAGATGGACTGACATTCBAAGGCCCTTGG
 TGTCTGAAGTCTCTGAATATGCAAGAAATGGAGTAAACGAACTTTATGGATGGAGCTTTTGGGGCTGAGCAA
 CATGGAAATTTTTCAGCTGGACCAATAACCACTTAACAGAGATTACCAAGGCTTGCCCTTACGGCTTGTGATGCT
 GCAGGAACTTCACTCTACGCAAAATGCCATCAACAGGATCAGCCCTGATGCTCGGGAGTTCTGCCAGAGCTCAG
 TGAGCTGGACCTAACTTTCACTCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCCTTAAGCTTACTAAATAC
 ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCGGGGGCTTCCAGTTTAAAGACTTT
 GGAATCTGAAGAACAATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTTCGGGCTTGACAACTGAG
 GCGACTGATATCTCAAGGAAATCGGATCGTCTTATTACTAAAAAGCCCTTCACTGGTTTGGATGCATTTGGAGCA
 TCTAGACCTGAGTGACACGCAATCATGTCTTTACAAGGCCAATGCATTTTCACAAATGAAGAACTGCAACAAT
 GCATTTAAATACNTCAAGCCTTTTGTGGATTTGCCAGTCAAAATGGCTCCCAAGTGGGTGGCGGAAACAACCTT
 TCAGAGCTTTGTAATGTCAGTTTGTGCCATCTCAGCTGCTAAAGGAAGAAGCAATTTTGTCTGTATAGCCAGA
 TGAGCTTTGTGTGTGATGATTCTTCCAAACCCAGATCACGTTTCAGCCGAAACACTCGGCAATAAAGGTTT
 CAAATTTGAGTTTCATCTGTCTCAGCTGCCAGCAGCATGATTCCCAATGACTTTTGTCTGGAAAAGACAATGAC
 ACTACTCATGATGCTGAAATGAAATATGACACACCTCCGCGCCCAAGGTGGCGAGGTGAGGAGTATACCA
 CATCTCTTCGGCTGGCGAGGTGGAATTTGCAAGTGAAGGAAATATGATGCTCATCTCCAACTCATCTTTGGTTT
 ATCTACTCTGTCAAGCCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGATGATCTCACAT
 CCGAGCTGGGGCCATGGACCGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCAAGATAGGCTTGGCAGAAAG
 TGGGGGCAAGACTTCCCAAGCTGCAACGGGAGAGACGATGATGATGATGATGATGATGATGATGATGATGATGAT
 GAT
 AACTCTGACTGTCTAGAAACCACTCATTTTTCGCCCACTGTTGGACCGAAGCTGTAACCAAGGAGAGAACAGC
 CGTCTACAGTGCAATTGCTGGAGGAAGCCCTCCCTCTAAACTGAACCTGAGCAAGATGATAGCCCATTTGTTGTT
 AACCGAGAGGCACTTTTTCGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGAATGCTGGGAA
 ATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTTGGCTCAGATGTGATCCCACTCCAG
 CTGCACTCCCTCAGATGACAGCCCATCGTTAGAGGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAGC
 CGTGGTTTGTCTGTGTGGTGGGCACTGCTGCTGTGGGTGGTCACTATATACCAACAAGGCGGAGGAATGAAGA
 TTGCACTATACCAACACAGATGAGACCAACTTGCACGACAGATATTTCTAGTTATTTGTGCATCTCAGGGAACGTT
 AGCTGACAGGAGGATGGGTACGTTGCTTTCAGAAAGTGAAGCCACCAAGTTTGTGCATCTCAGGTGCTGG
 ATTTTCTTACCAACAATGACAGTGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAGCTGTC
 CACAGATCTGTTCTTGTGCGTTTGGGATCCACAGGCCCTATGTATTGTAAAGGAAATGTGATATGGCTCAGA
 TCCTTTTGAACATATCATACAGGTGCACTGCTGCTGACCCCAAGAACAGTTTAAATGGAACAATGATGAGCCCACT
 CATAAAGAAAAAGAGTGTGATCCATGTTCTCATCTCTCAGAAAGATCCTGCGAACCGAGCTTTCAGTAATATC
 GTGGCTTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCAATGAAGACCTGGAATGAAAAATCTGTG
 TCTAAATGCTCTCTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTGGCTGCTCGATTAATCTTTTATGGG
 TACCTTTGAAAAAGCTCTCAGGAGACCTCAGCTAGATGCTATTCAAGCTTTGGACAGCCATCAGATTGTCAAGC
 AAGAGCTTTTATTTGAAAGCTTCTTCCCAAGCTTGGACTCTGGGTGAGAGGAAGTGGGAAGAAAGAACAG
 AGATTTTTCAGGAAGAAATCATTGTTACCTTTAAACAGACTTTAGAAAAATCAGAGCTCCAAATTTTCACTC
 TATGACTTGGACACAT**TAG**ACTGAATGAGACCAAGGAAAGCTTAACATACATCCTCAAGTGAACCTTTTATTA
 AAAGAGAGGATCTTATGTTTAAATGGAGTTATGAATTTTAAAGGATTAATAATGCTTTTATTTATACAGAT
 GACACCAATATACAAAAATGATGAAAAATTTTATATCTGGGAATGATGCTCATATAAGAAATACCTTTTAAACTA
 TTTTAACTTGTGTTTATGAAAAAGATCTTACGTAAATTAATGATATAAATCATGATTTTATGATTT
 TTATAATGCCAGATTTCTTTTATGGAAAAATGAGTTACTAAAGCAATTTTAAATAATACCTGCTTGTACCAATTT
 TTAATAGAGATTACTTCATTATTTTGCACATTTATTTTAAATAAATGTGCAATTTTGA

FIGURE 102

MVDVLLFLSCLLFHISRDPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSA
ITLLSLAGNRIVEILPEHLKEFQSLSETLDDLSSNNISELQTAFPAQLKYLKYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAIIPKMFKLPLQLQHLELNRRNKKIVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNNMELQLDHNNTETITKGWLYGGLMLQELHLSQNAINRISPDWE
FCQKLESLDLTFPHLSRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDQLKWLQWVAENNFOQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITTVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELHDAEMENYAHLRAGG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVMNLPSTKTPTMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSTAQN
SAGSISANATLTVLETPSFRLPLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVSDAGKYTCESNTLGTERRGNVRLSVIPTPTCDSPQMTAFSLDDDG
WATVGVIIVAVCCVVGTSLVVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLD
RQDGYVSSSESGSHHQVFTSSGAGFPLQHDSSGTCIDNSSSEADVEATDLFLCPFLGSTGP
MYLKGNYVSGDPFETYHTGCSFDPRTVLMHDYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGFGMKNLCLNKSSLDFSANPEPASVASSNSFMGTGFKALRRPHLDA
YSSFGQPSDCQPRAFYLLKAHSSPDLDSSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTTCTCTGGAAACCGAAGCGCAATGGATAAACTGATGTGCAAGAGAGAAGGAGAAG
GAAGCTTTTTCTTTGTAGCCCTGGATCTTAAACACAAATGTGTATATGTGCACACAGGGAGACTCAAGAAATGAAA
TAAACAGAGTTAGACCCCGGGGGTGGTGTGTTCTGCACATAAAATAAATACTTAAAGCAGCTGTTCCCTCC
CCACCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTCTATTTTTCTC
TATAAAGGAGAAGGTGAGCCAAGGAGATATTTTTGGAATGAAAGTTGGGGCTTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTTTTTCTTTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAAAGAAA
TTTCAGAGAGAAGATTGACCGCGGAGATGAGGCATTGATTGGGGAGAGAAACAGCAGAGCAGTGGGA
TTTGTGCTTATGTTGACTAAATGACGGATAATTGACAGTGGATTTTCTCATCAACCTCTTTTTTTAAAT
TTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAACCACTGGATTTCATCTGGATGTGGT
GTGATCAGTCTGAATATCAACTGTTTGAATTCAGAAGGACCAACACAGATAAAATTGAATGTTGAAACAAGAT
GACCTTACATCCACAGCAGATATGATAGTCTTAGTTTAAACAGGCCCTATTGACCCCTGCTGTGGTGTCT
CTGGCTCTTCAACTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACCTGCCCTCTGTGTGCTCTTGACAGCAA
CCAGTTCAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGGAGTTCGGATGGCATCTCCACCAACACAGGCT
CGTGAACCTCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCATCTGAGGCACTTGGAAATCCT
ACAGTGTAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTCAATGGTCTGGCGAACCTCAAACACTTGGGA
ACTCTTTGACAATCGCTTACTACCATCCGAAATGGAGCTTTTGATACTTGTCTAAACTGAAGAGCTCTGGT
GCGAAACCAACCATTGAAAGCATCCCTCTTATGCTTTTAAACAGAAATCCCTTCTTGGCGCGCATAGACTTAGG
GGAATGAAAAGACTTTCATACATCTCAGAAGTGCCTTTGAAGCTCTGTCCAATCTGGAGGATTTTGAACCTTGC
CATGTGCAACTTTCCGGAATCCCTAACTTCACCCGCTCATAAAATAGATAGGCTGGATCTTCTTGGGATCA
TTTTATCTGCCATCAGGCTTGCTCTTTCCAGGGTTTGATGCACCTTCAAAAATCTGTGGATGATACAGTCCAGAT
TCAGTGATTTGAACGGAATCCCTTTGCAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAAATACTTAAC
ATTACTGCTCTCATGACTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCAACACCTTTGGAAGT
TAACTGTGACATATCTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACAACAGCTTGTGTGGCCCGTG
TAACACTCTCCCAATCAAAAGGGAGGTACATTTGGAGAGCTCGACAGAAATTAATCTCAGATGCTATGTCTCGGT
GATTTGTGGAGCCCTCCAGACCTCAATGTCACTGAAGSCATGGCAGCTGAGCTGAAATGTGGGGCTCCACATC
CTTGACATCTGTATCTTGGATATCTCAAAATGAAACAGTCTGACACATGGGGCGTACAAAGTGGCGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTCAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAAGTAA
TTCCGTTGGGAATACTACTGCTTCAGCCACCTGATGTTACTGTCAGCAACCACTACTCCTTTCTTACTTTTC
AACCTGCAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACACAGATAACAAATGTGGGTCCCACTCC
AGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAAGTGCAGAGAGAAAACTT
CACCATCCCAAGTGAATGATATAAACAGTGGGATCCAGGAATGATGAGTCAATGAAGACTACCAAAATCATCAT
TTGGGTGTTTTGTGGCATCACACTCATGGCTGCAGTGATGCTGGTCAATTTCTACAAGATGAGGAAGCAGCACC
TCGGCAAAACCATCACCCCCCAAGGACTGTTGAAATATTAAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCCACTGCCATGCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAATCTCCCTT
CAACACACAAACCAAGTTAAACAAATAAAATCAATACACAGTTCAGTCAATGAACCGTTATTGATCCGAATGAA
CTCTAAGACAATGTACAAGAGACTCAAAATCTAAACATTACAGAGTTACAAAAAACCAACAAATCAAAAAA
GACAGTTTATTAATAATGACCAAAATGACTGGGTAAATCTACTGTTTCAAAAAAGTGTCTTACAAAAAACA
AAAAAGAAAGAAATTTATTTATAAAATCTATTGTGATCTAAGACGACAAAAA

FIGURE 104

MLNKM TLHPQQIMIGPRFNRLFDPLLVVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLNLHENQIQIIKVNSFKHLRHLEILQLSRNHRTIEIGAFNGLA
NLNLTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNRLYNLNLAMCNLREIPNLTPLIKLELDL SGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLER IHLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTGMYTCMVSNVSGN
TTASATLNVTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGTPVVDWETTNTVTTSLTPQ
STRSTEKFTTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTMPMESHLPMPAIEHEHLNHNYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCGCAGCGCTGCTCAAGCTGCAACTCTGTTCAGTGTGGCAGTTCCTTTCGGTTCCTCTGCTGTTTGGGGGCA
 TGAAGGGGCTTCGCGCGCGGGAGTAAAGAAAGAAATGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC
 GAGGGCGGGCGTGCACCTTCGGCTGGAAGTTTGTGCGGGGCCGAGCGCGCGCTGGGAGCTTCGGGTAGA
 GACTAGGCGCGTGGACCGGCTAGAGCGCGCCGAGCCTTCGTCGCGCGCGCGCGGGGTGGGGCTGCTGCTGTGCG
 GCGGTGCTGGGGCGCGCTGGCGGGTCCGACAGCGCGCGTGGCGGGAACTCGGCGAGCCCTCTGGGGTAGCCGCGC
 GAGCGCCATGCCCACTACCTCGCGCTGCTCGGGGACCTGCTGGACTGCAGTCTGTAAGCGGTAGCGCGCTCTT
 CCGGAGCACTCGCGCTCTGGGTGCTCGGCTGGACTTAAGTCAACAAGATTTCTTTTATCAAGGCAAGTTCC
 ATGAGCCACTTCAAAGCTTCGAGAAGTGAACATGAACAACAATGAATGGAGACATTTCACAAATCTGGGACCA
 GTCTCGGCAAAATATCACTTCTCTCTGCTGGAAACAGGATTTGTAATTTTGACAAATTTGGCCAAACCA
 CTCCTTTGTTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCCAAGATGTTTAAACTGCCCACTGCA
 CATCTCGAATTGAACCGAAACAAGATTAAATATGTAGATGGACTGACATTCGAAGCGCTTGGTGTCTCTGAAGTCT
 CTGAAAATGCAAGAAATGGAATTAACGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG
 CAGCTGGACCATACCTTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGTGATGCTGCAGGAATCTCAT
 CTCAGCCAAATGCCATCAAGAGATCAGCCCTGATGCTGGGAGTTCTGCGCAAGCTCAGTGAGCTGGAACCTA
 ACTTCAATCACTTATCAAGGTGATGATTCAAGCTTCTTGGCTAAGCTTACAAATACACTGCACTTGGG
 AACCAAGAGTCACTTCTGATTTGTGCTTCCGGGGCTTTCAGTTTAAAGACTTTGGATCTGGAAGAAC
 ATGAAATTTCTGACTATTGAAGACATGAATGGTGTCTTCTGGGCTTGACAACTGAGGCGAGTGAATCTC
 CAGGAATTCGATCGCTTCTATTACTAAAAGGCTTCACTGGTTTGGATGATTTGGAGACTCTAGACCTGAGT
 GACACGCAATCATGTTTTCACAGGCAATGCATTTCAAAATGAAGAACTGCAACAATGGCAATTAATATA
 TCAAGAGTTTGGGCTGTCAGCTTAAATGGCTCCCAAGTGGTGGCGGAAACAATCTTTCAGAGCTTTGTA
 AATGGCAATGTGGCCATCTCAGCTGCTAAAAGGAAGAGCATTTTGTCTGTAGCCAGAGTGCTTTGTGTGT
 GATGATTTTCCCAACCCAGATCAGCTTCAAGCTGAGCAAGAACAGTGGCAATTAAGGTTTCCAATTTGAGTTTC
 ATCTGCTCAGCTGCGAGCAGCAGTGAATCCCAATGCACTTTGCTTGGAAAAAGCAATGAATCTGCAATGAT
 GCTGAAATGGAATTTATGCAAGCACTCTCGGGCCCAAGTGGCGAGGTGATGAGATATACCACTCTCTCGCTG
 CCGAGGTGGAAATTTGCCAGTGAGGGGAAATATCAGTGTGCTCATCTCAATCACTTGGTTTCCGTACTCTGTC
 AAAGCCAGCTTACAGTAAATGTCTTCTCTCATCAACCAAGCCCCATGGATCTCACTCATCGAGCTGGGCGC
 ATGCCAGCTTGGAGTGTGCTGTGCTGGGGCACCAGCCCTCAGATAGCTGGCAGAGGATGGGGGACAGAC
 TCTCCAGCTGACGGGAGAGACGATGATGTGATGCGCGAGGATGACGTGTTCTTTATCGTGGATGGAAGATA
 GAGGACATTTGGGTATACAGCTGCACAGCTCAGACAGTGCAGGAGATATTTCAAGCAATGCACTCTGACTGTC
 CTAGAAACCACTATTTTTCGGGCCACTGTGGACCGAAGCTGAACCAAGGAGAAACAGCGCTCTACAGTGC
 ATCTCTGGAGGAAGCCCTCCCTTAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACT
 TTTTTCGACGACCAATCAGCTTCTGATTATTTGTGACTCAGATGTGAGTGTCTGGGAAATACACAGTGTGAG
 ATGTCTAACACCTCTGGACTGAGAGAGGAAAGTGGCCCTCAGTGTGATGCCCACTCCAACTGCGACTCTCCCT
 CAGATGACAGCCCTCTGCTAGACGATGACGATGACGATGACGATGACGATGACGATGACGATGACGATGACGAT
 GTGGTGTGCTCACTGCTGGTGGTGTGATCATATACACCAAGGCGGAGGAATGAAGATTTGCAGACTTACC
 AACACAGATGAGACCACTTGGCAGCAGATATTCTAGTTATTTGTGATCTCAGGGAACGTTAGCTGACAGGCG
 GATGGTACGCTGCTTCAAGAAAGTGAAGGCCACACAGTTTGTGATCTCTCAGGTGCTGGATTTTCTTACCA
 CACATCACTGATGAGGACCTGCAATATTGACAAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTCT
 CTTTGTGCTTTTGGGATCACTGAGCTTATGATTTTGAAGGGAATGTGATGGCTCAGATCTTTTGAACCA
 TATCATACAGTGTGAGTCTGAGCAGCAAGAACAGTTTAAATGGACCACTATGAGCCAGTTCATGAAGAAAG
 GAGTGTACCCATGTTCTCATCTCTCAGAAGAACTCTGCAAGCGGAGCTTCAGTATATATCTGTGGGCTTCACAT
 TGTGAGGAGCTCTTAACACTAGTTACTCTCAAAATGAAGGAGCTGGAAATGAAATATCTGTGCTTCAAGAGTCC
 TTTTATGATTTTATGTCAGAAATCGAGGCGAGCTGGTGTGCTCGAGTAAATCTTTCATGGGTCAGCTTTGGA
 GAGCTCTCAGGAGACCTCAGCTAGATGCTTATCAAGCTTTGGACGCAATCAGATTTGTGAGCCAGAGCTCTTAT
 TTGAAGGCTCATTTTCTCCAGACTTGGACTCTGGGTGAGAGAGATGGGAAAGGAAGACAGATTTTCAGGAA
 GAAATACCATTTTGAATCTTTTAAACAGACTTTAGAAACTACAGGCTTCAAAATTTTCAGTCTTATGACTTGGAC
 ACAAGACTGATGAGACCAAGGAAAGGCTTAAACATACTACCTCAAGTGAATTTTATTTAAAGAGAGAGAAAT
 CTTATGTTTAAATGGAGTTATGAAATTTTAAAGGATAAAATGCTTTATTTATACAGATGAACCAAAATATAC
 AAAAGATGATGAAATTTTATACCTGGGAATGATGCTCATATAAGAAATACCTTTTAAACTATTTTAACTTGT
 TTTTATGCAAAAGATGATCTACGTAATTAATGATATAATCATGATTTTATGATTTTATGATGCGAGA
 TTTCTTTTATGAAATGAGTTACTAAAGCATTTTAAATTAATACCTGCTGTGACATTTTAAATGAGAGT
 ACTTCATATATTTTGCATATATTTTAAATAAATGTGCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLDDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETTDLSSNNISELQTAPPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNISAI PPKMPKLPQLQHLELNRRNKIKNVDDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNNTETITKGWLYGLMLQELHLSQNAINRISPDWAEFC
QKLSLDDITFNHLSRLDDSSFLGLSLNLTLIHIGNNRVSYIADCAFRGLSSSLKTLDLKNNIS
WTIEDMNGAFSSGLDKLRLRLQGNRIRSI TTKAFTGLDALEHLDSLDAIMSLQGNAFSQMK
KLQQLHLNLTSLCCQQLKWLQWVAENNFQSPVNASCAHPQLLKGRSIFAVSPDGFVCDFF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNEILLHDAEMENYAHLRAGGGE
VMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVKAKLTVNMPLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGQDTFFAARERRRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSLVVTTERHF
FAAGNQLLIIVDSVSDAGKYTCEMSNTLTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIIAIVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLLADRO
DGYVSSSESGSHHQFVTSSGAGFPLPQHDSSSGTCHIDNSSSEADVEAATDLFLCFFLGSTGPMY
LKGNVYGSDDPFETYHTGCSDPDRTVLMDHYEPSYIKKKECYPCSHPSSESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPPAFYALKHSSPDLDGSGSEEDGKERTDFQENHICTFKQTLNRYRTPNFQSYDLDIT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACCTTGCCTCGCGGAGAGCGCCGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAG
 TGGGGGAGCGCGTTTGGCCTTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGAAGCTGTGGTCTTGGCC
 CTGCTTCCACGAGCGCCACACTGTGTGTGAACCGGAGAGCCCTGGGTGCTCCCTTATCCCTCTTTATATATA
 GAAACCTTTCCACACTGGGAAGCGCAGCGCGAGGCGAGGAGGCTCATGGTGAGCAAGGAGGCGCGCTGATCTGCAG
 GCGCACAGCATTTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGCGGAGAGCGAGAACAGCTGCTCTGGT
 TCCATCAGCCTTGGCGCCGACGCGCATCTGACTCGGCAACCCCTGCAGGACCAATGSCCCAGAGCGCGGTGCTGC
 TGCTCTGTCTGTGCTGCTCGGACACAGCTGCACTGGAACCTGTGCTTGCCTGTGAGGGGCCCAAGATTTGGCCGAA
 GTGGCGCCACAGCTCAGCCCCGAAAGAAACGAATTTGCGAGAGAGAGCGCGGTGCTGGTACTGAGCCTGAGG
 AGCCCGGCTGCGCCAGCGCGCTCAGCTGCCCGGAGACTGTGCTGTTCCAGAGGGCGCTCGTGTGAGCTGTGTG
 GCGGTATTGACTCTGCTGAGTTTCCCGGGGACTGCTGAGCACCAACCACTATCTCTGAGAAACAAACAGC
 TGGAAAGAGATTGACCTTGAGAGGCTCTCCCGCTGCACCGCTGGAGACACTGAACTGCAAAACAACCGCTGA
 CTTCCTCGAGGGCTCCGAGAGAAGGCGTTTGAGCATCTGACCAAACCTCAATTACCTGTACTTGGCCAAATAACAGC
 TGACTTTGGCACCCCGCTTCTTGCACAAACGCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT
 ATGGGCTCAACTTTGGCGAGAAGCCAAACTTGAGGTCTGTGTACTCTGCACAAACAAAGCTGGCAGACCGCGGGC
 TGCCGGACCAACTGTTCAACGCTCCAGCAAGCTGAGGCTCTCATCTGTCCAGCAACTTCTCTGCGCACGCTGC
 CCAAGCACTGCGCGCTGCCCTGTACAAAGCTGCACCTCAAGAACCAACAGCTGGAGAGAAGATCCCCCGGGGCT
 TCAGCGAGCTGAGCAGCTGCGCAGCTATACCTGCAAGAACACTCACTGACTGACGAGGGCTGGACCAACGAGA
 CTTCTTGGAAAGCTCTCCAGCTGGAGTACTGGATCTGTCCAGCAACCACTGTCTCGGGTCCAGCTGGGCTGC
 CGCGCAGCTGTGCTGCTGCACTTGTGAGAAGAACGCCATCGGAGGCTGGAGCGCAATGTGCTGACCCCACTCC
 GCAGCTTGGAGTACTGTGCTGTCACAGCAACAGCTGCGGGAGCAGGGCCTCAACCACTGGCTTCCAGGGCT
 TCAAGCGTTGTACACGCTGCACTGTACAAACAGCGCTGGAGCGGCTGCCCACTGGCTGCTCTGCGCGCTGC
 GCACCTTCATGATCTGCGACAACAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACTACTTCTCTGGAGG
 AGCTCAACCTCAGCTACAACCGCATCACAGGCCACAGGTGCACCGGACGCTTCCGCAAGCTGCGCTGTGCTGC
 GCTGCTGGAACTGTGCGGCAACCGGCTGCAACGCTGCCACTTGGGCTGCTCGCAATGTGCTATGTGTGAAGG
 TCAAGCGCAATGAGCTGGCTGCTTGGCACAGGGGGCTGCGGGGCTGCTGAGCTGCTGAGCTGTACCTCA
 CCAGCAACCGACTGCGCAGCGAGCCCTGGGCCCCGCTGCTGGGTGGACTTCCGCCATCTGACAGTGTCTGGACA
 TCGCCGGGAATCAGCTCACAGAGATCCCGAGGGGCTCCCGAGTCACTTGAATACCTGTACTGCAAGAACAA
 AGATTAGTGGGTCGCCCGCAATGCTTCGACTCCACGCCCACTCAAGGGGATCTTCTCAGGTTTAAACAAGC
 TGGCTGTGGGCTCGGTGGACAGTGCTTCCGAGGCTGAAGCACTGCAAGTCTTGGACATTGAAGGCAACT
 TAGAGTTTGTGTGACATTTCAAGGACCGTGGCCGCTTGGGGAAGGAAAGGAGGAGGAGAGAGAGGAGGAGG
 IAGGAAGAGGAACAGAGATAGTGACAAAGGTGATGAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTCTGC
 AGCACAGCTGTGTGCTGTGAGCCCCCACTTGCCTGTCTCACACAGACACCCAGCTGCACATGAGGGA
 TCCCACTGACACGGGCTGACACAGTCTCATATCCCAACCCCTTCCACGGGTGTCCACGGCCAGACACATGC
 ACACACATCACACCTCAAAACCCAGCTCAGGCCACACAACTACCTCCAAACCCACACAGTCTCTGTACAC
 CCCCACACTACCGTGCACGCGCTCTGAATCATGCAAGGGAAGGGTCTGCCCTGCCCTGGCACACACAGGCAACCA
 TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCAACACACACATGCACCAAGTCTATGTGGAA
 CAGCCCTCCAAAGCTATGCCACAGACAGCTCTTGCCTCCAGCAGAACTCAGCATAGCAGCTCGCCGTCTGCCCT
 GTCCATCTGTCCGTCCGTCTCCCTGGAGAAGACACAAGGATTCATGCTCTGTGGCCAGGTGCTGCCACCTCT
 GGAATCACAAAGCTGGCTTTTATCTCTTCCATCTCTATGGGACAGGAGCTTCAAGACTGCTGGCTGGCC
 TGGCCCACTCTCTCCAGAGTGTGGGCACTCTGCTGAAGAGTCCCTCCCTGCCACGCTTGGCAGGACA
 CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGACAGATGGGAGAGCCCCCTGGGTGCTGTGGGCTTGGG
 CAGGAGTGAAGCAGGATGATGGGCTGGGCTGAGCAGGAGGAAGACCCAGCTGCACTTGGAGACACCTTT
 GTTCTTCAGGCTGTGGGGAAGTTCCGGGTGCTTTATTTTATTTTATTTCTTGAAGGAAAAAATGATAAAAAT
 CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAAGCATTATCCCTATCCCTGCAAAAAA

FIGURE 108

MEGEEAEQPAWFHQFWRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPFVLAVRAPGFGRS
GGHSLSP EENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVD CGGIDLREFPGDLF
EHTNHLSLQNNQLEKIYPEELSR LHRLETLNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLT KIYGLTFGQKPNLRSVYLHNNKLADAGLPD NMFGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKI PPGAFSELSSSLRELYLQNNYLTDEGLDN
ETFWKLSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEEILNSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRR LKHLQVLDIEGNLEFGDISKD
RGR LGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGGCGCGCGCAGCAGACCTGCTCCGGCGCGCGCTCGCGCTGTCTCTCGGGAGCGGCAG
 CAGTAGCCCGGGCGGCGAGGGCTGCGGGCTTCCTCGAGACTCTCAGAGGGCGGCTCCCATCGGGCGCCACCAACC
 CAACCTGTCTCTCGCGCGCCACTGCGCTGCGCGCCAGGACCCGCTGCCCAACATCGGATTTTCTCTGGCGCTGGT
 GCTGGTAICTCTCGCTCTACCTGCAGGCGCGCGCCGAGTTCGACGGGAGGTGGCCAGGCAATAGTGTGCATCGAT
 TGGCCTATGTCTGTTATGTGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGCAGCG
 TGTGTGGCCAAACCAATGAGCAATGATGGTGAATGTATCGGGCCAAACAAAGTGCAAGTGTGCATGCTGGTGTATGCTCGG
 AAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGGAAGCCCGCGCCCTGTAAGCAGCAGGTGCATGAACACTTA
 CGCGAGCTACAAGTGCTGCTACTGCTCAACGGATATATGCTCATGCGCGGATGGTTCCTGCTCAAGTGGCCCTGACCTG
 CTCATGTGGCAAACTGTGATGTAGTGTGTGTAAAGGACAAATACGGTGCACAGTGCCTCATCCCTCGGCTGGCTG
 GCACCTGGCTCTGATGGGAGGACCTGTGTAGATGTGTGATGAATGTGCTACAGGAAAGAGCTCTTCTGCCCTAGATT
 TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTAATAAGGCTTCGATCTCATGTATATTGGAGG
 CAAATATCAATGTGCATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAAGCTTTGCTCGATGTTATAA
 CGTACGTGGTCTCAAGTGCATAATGTAAAGGAAGATAACAGGGTGTGAGTGAATGCTGTGTGTATATCCCAAA
 AGTTATGATTGAACCTTCAGGTCCAATTGATGTACCAAAGGGAATGGTACCAATTTAAAGGGTGACACAGGAAA
 TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACCACTATATCTCTCTTATTATTACCAA
 CAGGCTACTTCTAAGCCAACACAGACCTACACCAAAGCCAACCAATTCCTACTCCAACCAACCACCACC
 CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAAACCCAGAAAGGCCAACCAACCGGACTGACAACTATAGC
 ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGACCTCAGAAACCCAGAGG
 AGATGTGTTGAGTGTCTGGTACACAGTGTGAATTTTGACCAATGGACTTTTGGGATGGATCAGGGAGAAAGACAA
 TGACTTGCAGTGGGAACCAATCAGGGACCCAGCAGGTGGACAAATCTGACAGTGTCCGCGACCAAGCCCCAGG
 GGGAAAAGCTGCAGCCTTGGTGTACTCTCGGCGCGCTCATGCAATCAGGGGACCTGTGCTGTCTATTGAGGCA
 CAGGTTGACGGGCTGCACTCTGGCACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
 GGGAGAAATGTTGGGCCATGGCTGGAGGCAAAACAGAGTCACTTGCAGGGGCTGACATCAAGAGCGAATCACA
 AAGATGTAATAAGGGTTGGAAAAAAGATCTATGATGGAATAATAAGGAACTGGGATTTAGAGCTTGAGAGA
 AGAAGACTGAGGGGCAACCAATGATGTTTCAAGTATATGAAGGGTTGGCAGAGAGGGTGGCGACCAAGCTGT
 TTCTCCATGTGCACTAAGAAATAGAACAGAGGAACTGGCTAGACTAGAGTAAAGGGAGCAATTTCTGGCAGG
 GGCCATTTGATAGTAATCTCATAAAAAAAGAGTGTGAAAACTCAGTATCTCTCTCTTTCTAAAAAATTAGA
 TAAAAATTTGTCTATTAAAGATGGTTAAAGATGTTCTTACCAGGAAAGTAACAAATTAAGAAATTTCCCAAA
 AGATGTTTGTATCTACTAGTAGTATGACAGTGAATCTTTAGAACTAAATAATTTGGAACAGGCTTAATTTAGG
 CATTTCCCTCTGACCTCTTAATGGAGAGGGATTGAAAGGGGAAGAGCCCAACCAATGCTGAGCTCACTGAATA
 TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAAAGGAACTATTATTCCCAATGAGAGTATGATGGAC
 AGATATTTTAGTATCTCAGTAATGTCTTCTAGTGTGGCGTGGTTTCAATGTTTCTTCATGTTAAAGGTATAAGCC
 TTTCAATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTTCAGAGAG
 ATTTTCTCGGGTGCAATCTCTGCTTCTGTTGTGACAAAGTTATCTTGGCTGCTGAGAAAAGTGGCCCTGCCCC
 ACACCGGAGACCTTTCTTCACTCATCAGTAGATTGAGTTTCTTATCAATTTGGAATCTCCCAAGGTCCAC
 AGAACAGTAATATTTTTTGAACAATAGTACAAATAGAAGTCTTCTGTCAATTAACCTGGTAAAGGAGGGCTGG
 AGGGGGAATAAATCATTAAGCCTTTGAGTAACCGGCAAGATATATGGCTGTAGATCCATTTTAAATGGTTTCAAT
 TCCTTTATGGTCATATACTGCAGCTGAAAGTGAAGGGGAAAAATAATGAAAAATTTTACTTTTCGATGCCAA
 TGATACATTGCATAAATGATGGAAGAGTATCCAAAGTACTGTATAACATCTGTGTTATTTAATGTTT
 CTAAAAATAAAAAATGTAGTGTGTTTCCAAATGCCATAAAAAACAAATATTTGTAATTAACAACTGTAGTAAT

FIGURE 110

MDFLLLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVQCQ
RCKKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKGQIRCQCPSGLHLAPDGRTCDVDDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVVRSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGNTILKSGDTGNNNWIPDVGSTWWFPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTTGLTTIAPAASTPPGGITVDN
RVQTDPPQKPRGDFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAPAGG
KAARLVLPGLRMLHSGDCLCSFRHKVTGLHSGTLQVVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGGCCCTTTAGATTGTGA
AATGTGGCTCAAGGTCCTTCAACAACCTTTCTTTCTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGTGAGAGACCCCA
CACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTTGACTTGGAATACC
AACACAAGTTCACCATGATGCCACCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACCTCTATCTGCCAGTCA
GAAGATACAAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGAGATTATCCTCTCCCT
CTGGGCGTGTGGAGTATGTGGGGAACATGACCTGACATGCCATTGGAAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCTTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTGAGTGAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCGCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAACAAATGGACTATGTGTGCTGTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTTTACAGTTATCATCACTTCCGTAGGACTGGAGAAAGCTTG
CACAGAAGGAAAAATCATTTGTACCTTTAGCAAGTATAAAGTGAATATCACTATTTTGTATT
ATATCCAAAGTGCTCTTCTCTTCTATGAAAAAATATCAACCCCTACAAGATTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTTCAGGCCATTGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTGAGCAGATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTTATTCCTTTTACA
TGCAGATAGAGGCATTTATGCAAAATGAACTGCAGGTTTTTTCAGCATATACAAATGTCTT
GTGCAACAGAAAAACATGTGTGGGAAATATTCCTCAGTGGAGAGTCTGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCTCTATAAGTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACATTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAACCTTTACATTGTTTCGATTTTTCAGCAGACTTGTGTTTATTAATTTTATTTAGTG
TTAAGAAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACATAGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTTGAGAAGACTTGTGAACACTTAAAGAAATGACTATTAAAGTCTTATTTTAA
TTTTTTTCAAGGAAAGATGGATTCAATAAAATTTATCTGTTTTTGTCTTTTAAAAAATAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLKGSVNKSVVPDLEYQHKTMMPPNASLLINPLQFPDEGNIVKVNIQNGTSLASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEIDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVITIISVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDPGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGCGCCCTCCGGGAGTCTTGCAAGTTCCCCTGGCAGTCTCGGTGCTGTT
GCTTTTGGGGTGCTCCCTGGGAGCGACGGGCGGCGAGCAACGTTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTTGGTGCCTGCT
TGTCAAATCTTCAACCGGAATGGGAAAGTTTGTGGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCAATTGTAAAGATGTTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCGTTTCATCATG
GTTTGTGTCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGTCTTAGCAACTCTGTTTTCCGGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCCTTGTCTTCAAAAAGGCGCAGACCACGCCATACCCATACCCCTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGCGGATGAAGAA
GATGTTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAACAAGAGACTTTCCACAGATGC
CATAAGACACGCTCTCTGGGTCCATCATTTGGCCACAGATAAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTTGATAAAAAACAGAAGATTGATCATTTTGTTTGGTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCACTCTAGATTGTCAATAAATTGAAGAGTCTA
CATTCAGAACATAAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAAATTTTGA AAAATCGTGCCAAGCAATAAGATTATGATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTTACATTTCCCAAGTATTGCAATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTGTATATAAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCATAAATGGGAAGTTTGCCCATTTGCTCAAG
AAATGTGATTTTCAGTGACAATTTCTGTGCTCTTTTAGAGGTATATCCAAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAACCTACCTTACATTAATTAATACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTAAGTTTCATGGTATTTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTTGTATTTTCTTACTTACTATGGGTTACATTTTATTTT
CAAATTTGGATGATAATTTCTTGAAACAATTTTTATGTTTTTAGTAAACAGTATTTTTTGT
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAAATTGAACAATCTGTTGTAATTTAAAT
TTGGCCACTTTTTTCAGATTTTACATCATTCTTGCTGAACCTTCAACTTGAAATTGTTTTTT
TTTCTTTTTGGATGTGAAGGTGAACATTCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGA AAAATCAAGAAGCTTAATATAAAAGTTTGCAATCTACTCAGGAAAAAG
CATCTTCTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTTCTTAATGTAT
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACAATTTTATATTTTTTAAAGACAA
ACTTCAATATTCTCTGTCTTCTTCTGACTGGTAATATTGTGTGGGATTTCACAGGTAAAA
GTCAGTAGGATGGAACATTTTGTGTATTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAGAGGGGAAATCATAAATACAATGAATCAACTGACCAATACGTAGTAGAC
AATTTCTGTAATGTCCCTCTTCTTCTAGGCTCTGTTGCTGTGTGAATCCATAGATTTACAG
TATCGTAATATACAGTTTTTCTTAAAGCCCTCTCCTTTAGAAATTTAAATATTGTACCATT
AAAGAGTTTGGATGTGTAACCTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAACCT
TTCTAACCACTTCATTAAAGCTGAAAAA AAAAAAAAAA

03904766.071251

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFIISKWKSIIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCT
 CTGTGTGCCAGAAACCGCAAGCAGTTGTCTAAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
 AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCTGGAACCTCGGGTGTCTGC
 ATTGCTGATGGCCTGGTTTGGTGTCTGTGAGCTGTGTGCAGGCGGAATTCCTCACCTCTATTG
 GGCACTGACTGACCTGATTATGACAGAGAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGTGTAGGGGTACCTGGCTCACCCCTGTGAATGCCTACAACTGG
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGTGAGGACTCAGCTGCA
 GGTTTTATGCCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCGA
 GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCCTGTCTC
 TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAGAGGCA
 TCTATGAGAGGCCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGTGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
 TCGTCAGGTACTACGATGTCTGTCTGATGAGGAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGACAGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCCCTCACTGTCGCCAGCTA
 CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAAATTGTTACAGGTTGCAAAAT
 TATGGAGTGGGAGGACGATGAACCCGCACTTCGACTTCTTAGCGCACCCTTTGACAGCGG
 CCTCAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTTGGCCCTAAGAAGGGTACAGCTGTG
 TTCCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCTTCTCTGGTC
 CTTACGCCATGTCAACGTGACAGACACCTTTGTATGTTCTTCTGTATGTTCTTATCAGGCT
 GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCACTATAGGGCGACTCCTGT
 GTGACTGAAGTCCAGCCCTTCCATTACGCCCTGTGCCATCCCTGGCCCACAGGCTAGGATCA
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTTCAGTGAACCAAGTTCTGTACCTTGTTTACATGTTTGTTTTAT
 GGCATTTCTATCTATTGTGCTTTACCAAAAAATAAAATGTCTCCACGAGAAAAAAA

GCGAGTGTCCAGCTGCGGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCT

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDELVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLDQTYRLDPGTISRGEPLGTYQAMLSVDDCFGMGRSAYNEGDIYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVLYLPERDVYESLCRGEVGLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMRQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAATWPKKGTAVFWYNLLRSGECDYR
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTTCTCTCTCTTTTGTAGTGAAGACAGACCATAATCCAGCTGTGAGTGAAATGATTGT
 TTCAATTATTACCGTTTGGCTGGGGTGTAGTTCGACACCTTTCACAGTTTGAAGACAGGCAGAGGAGTTGTGA
 AGACAGGACAATCTCTCTGGGATGCTGGTCTTGGAAAGCCAGCGGGCTTGTCTGTCTTTGGCCCTCATTTGACCC
 CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGGCCATCAATCCATTGATCTCTTAGGGCTGTGCC
 CCTGGGGCACCCACTTGGCAGGGCCTTACCACATGCGACTGAGCTCCCTGTGTGGCTTGTCTGGCGCCAGCGCTTC
 CCCCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTGAGCCCTCTGCGGTTTCTCGATTCAGGGGGAGGGAGAAG
 ATCCCTGTGTGCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTTCGAGAGCTCGGCTAGACCAAAGTG
 ATGAAGACTTCAAAACCCGGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
 GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGTGTGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA
 CTTTGGCCGTGGCTGTGAACCGTACGCTGGCCCTCACTTCCCTCGGTACTCTACTTCACTGGGCAGCGGGGG
 CCGGGCTCCAGCAGGGATGCGAGTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTCCAGAGCCCTGC
 GCCACCTTCAACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGAGGATGACACATATGTGCAGGCC
 CCGCCTGGCAGCCCTTGTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGACAGGAGTTCAATTG
 GCGCAGGCGAGCAGGCCCCGTACTGTCTAGGGGGCTTTGGCTACCTGTGTGTCAGGAGTCTCTGCTTCTGCTGC
 GGGCACTCTGGATGGCTGCCAGGAGACATTCTCAGTGCCGTCCTGACGAGTGGCTTGGACGCTGCCCTCATTG
 ACTCTCTGGGCGTGGCTGTGTCTACAGCACCAGGGGCGAGGATATCGCTCATTTGAACTGGCCAAAATAAGGG
 ACCCTGAGAAGGAAGGGAGCTCGGCTTCTGTAGTGGCTTCCGCTGCACTCTGCTCCGAAGGTACCTCATGT
 ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAAGAACTGCAAGCTCAGA
 TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCGGGCTGAGCTGGCCCGTTGGCTCTCCCTGCTCTCTTTCA
 CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTTCACAGAGCAGCACACCTTCTCTCTGAGATGGGG
 CTCCCAAGTGCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCTGAGGCTGCTCTGAGCAGCTCA
 ATCGGCGTATCAGCCCTGCGCTGCGCTCCAGAAAGCAGGACTGCTCAACGGCTATCGGCGCTTCAGACCCAGC
 GGGCATGGAGTACACCTCGGACTGCTGTTGGAATGTGTGACACAGGCTGGGCACCGCGGGCGCTGGCTCGCA
 GGGTCAGCTGCTGCGGCGCTGAGCGCGGTGGAATCTTACCTATGCCCTATGTCATGAGGCCACCGGAGTCA
 AGCTGGTGTGCCACTCTCGTGGCTGAAAGCTGCTGAGCCCGGCTTCTCGAGGCGTTTGACCCAAATGTCC
 TGAAGCCACGAGAACATGATTGCTCAACCTGTTGCTGTCTACGGGCCACGAGAAGGTGGCGTGGAGCTCCAG
 ACCATTCTTGGGGTGAAGGCTCGAGCAGCGGAGTTAGAGCGACGATACCTTGGGACGAGGCTGGCTTGGCTCG
 CTGTGCGAGCAGGGCCCCCTTCCAGGTTGCACTCATGGACGTGGTCTCGAAGAAGCACCTTGGGACACTCTCT
 TCTTCTTACACCGTGTGGAACAAGGCTGGGCGGAGGCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
 GGCAGGCTCTTTCCAGTCCATTTCAGAGGTTCAATCTGCGCTGTACACACAGAGATCACC CCCAGGGCCCC
 CGGGGCTGGCCCTGACCCCCCTCTCCCTCTGTGTGCTGACCCCTCCCGGGGGGCTCTATAGGGGGGAGATTG
 ACCGCGAGGCTCTCTGCGAGGGCTGCTTCAACGCTGACTACTTGGCGGCCGAGCCCGGCTGGCAGGTGAAC
 TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCCTCGGGTTCTCAGGGCTCC
 ACCTCTTTCGGGGCTGAGCCAGGGCTGGTGCAGAAATTCTCCTGCGAGACTCAGCCCCAGCGCTCAGTGAAG
 AACTCTACCCGCTGCGGCTCAGCAACTGGAGGGGCTAGGGGGCGTGCCAGCTGGCTATGCTCTCTTGT
 AGCAGGAGCAGGCCAATAGCACTAGCCCGCTGGGGGCCCTAACCTCATTACCTTTCCCTTGTCTGCTCAGCC
 CAGGAAGGGCAAGCAAGATGGTGGACAGATAGAGAAATTGTGCTGATTTTTTAAATATGAAAATGTTATTAA
 ACATGTCTCTG

FIGURE 118

MRLSSLLALLRPALEPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPDSSRARLSD
QSDDEFKPRIVPYRDPENPKYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVS HGDERP AWMSETLRHLHTHFGADYDWWFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPD EWLGRCLIDSLGVGCVSQHQGGQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLT VLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCP LQGASRADVGDALETALEQLNRRYQPRLR FQKQRL LNGYR
RFD PARGMEYTTDLLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP LL
VAEAAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGADPDLGVKAAAAELERRY PG
TRLAWLAVRAEAPSQVRLMDVVSKHPVDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGDPDPPSPGADPSRGAPIGGRFDRQASAE GCFYNADYLAA
RARLAGELAGQEEEEALEGLEVM DVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQE QANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,

399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,

558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTGCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAA
TGCACCACCATGAGCATCATCACTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCCTCAGTTCTGAAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACATG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAATCTGTTGGGCTTTCTATTAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTACTTTTAAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACGCCTTAGGGCATTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAAGAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTTAAACACATGAACATTGTAAATG
TGTGGAAGAAGTGTTTAAAGAATAATAATTTTGCAATAAACTATTAATAAATATTATAT
GTGATAAATCTAAATATGAACATTAGAAATCTGTGGGGCACATATTTTGCTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAATGATATCTCTAGTTGTGAATT
TGTGATTAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGTCCTTCTCAAATGTACAACCTAAGCACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLSWAAVKETWTKHCDKAEPFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPQGGMIWKISEDQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

Fig. 1	Fig. 2	Fig. 3	Fig. 4	Fig. 5	Fig. 6	Fig. 7	Fig. 8	Fig. 9	Fig. 10	Fig. 11	Fig. 12	Fig. 13	Fig. 14	Fig. 15	Fig. 16	Fig. 17	Fig. 18	Fig. 19	Fig. 20	Fig. 21	Fig. 22	Fig. 23	Fig. 24	Fig. 25	Fig. 26	Fig. 27	Fig. 28	Fig. 29	Fig. 30	Fig. 31	Fig. 32	Fig. 33	Fig. 34	Fig. 35	Fig. 36	Fig. 37	Fig. 38	Fig. 39	Fig. 40	Fig. 41	Fig. 42	Fig. 43	Fig. 44	Fig. 45	Fig. 46	Fig. 47	Fig. 48	Fig. 49	Fig. 50	Fig. 51	Fig. 52	Fig. 53	Fig. 54	Fig. 55	Fig. 56	Fig. 57	Fig. 58	Fig. 59	Fig. 60	Fig. 61	Fig. 62	Fig. 63	Fig. 64	Fig. 65	Fig. 66	Fig. 67	Fig. 68	Fig. 69	Fig. 70	Fig. 71	Fig. 72	Fig. 73	Fig. 74	Fig. 75	Fig. 76	Fig. 77	Fig. 78	Fig. 79	Fig. 80	Fig. 81	Fig. 82	Fig. 83	Fig. 84	Fig. 85	Fig. 86	Fig. 87	Fig. 88	Fig. 89	Fig. 90	Fig. 91	Fig. 92	Fig. 93	Fig. 94	Fig. 95	Fig. 96	Fig. 97	Fig. 98	Fig. 99	Fig. 100	Fig. 101	Fig. 102	Fig. 103	Fig. 104	Fig. 105	Fig. 106	Fig. 107	Fig. 108	Fig. 109	Fig. 110	Fig. 111	Fig. 112	Fig. 113	Fig. 114	Fig. 115	Fig. 116	Fig. 117	Fig. 118	Fig. 119	Fig. 120	Fig. 121	Fig. 122	Fig. 123	Fig. 124	Fig. 125	Fig. 126	Fig. 127	Fig. 128	Fig. 129	Fig. 130	Fig. 131	Fig. 132	Fig. 133	Fig. 134	Fig. 135	Fig. 136	Fig. 137	Fig. 138	Fig. 139	Fig. 140	Fig. 141	Fig. 142	Fig. 143	Fig. 144	Fig. 145	Fig. 146	Fig. 147	Fig. 148	Fig. 149	Fig. 150	Fig. 151	Fig. 152	Fig. 153	Fig. 154	Fig. 155	Fig. 156	Fig. 157	Fig. 158	Fig. 159	Fig. 160	Fig. 161	Fig. 162	Fig. 163	Fig. 164	Fig. 165	Fig. 166	Fig. 167	Fig. 168	Fig. 169	Fig. 170	Fig. 171	Fig. 172	Fig. 173	Fig. 174	Fig. 175	Fig. 176	Fig. 177	Fig. 178	Fig. 179	Fig. 180	Fig. 181	Fig. 182	Fig. 183	Fig. 184	Fig. 185	Fig. 186	Fig. 187	Fig. 188	Fig. 189	Fig. 190	Fig. 191	Fig. 192	Fig. 193	Fig. 194	Fig. 195	Fig. 196	Fig. 197	Fig. 198	Fig. 199	Fig. 200	Fig. 201	Fig. 202	Fig. 203	Fig. 204	Fig. 205	Fig. 206	Fig. 207	Fig. 208	Fig. 209	Fig. 210	Fig. 211	Fig. 212	Fig. 213	Fig. 214	Fig. 215	Fig. 216	Fig. 217	Fig. 218	Fig. 219	Fig. 220	Fig. 221	Fig. 222	Fig. 223	Fig. 224	Fig. 225	Fig. 226	Fig. 227	Fig. 228	Fig. 229	Fig. 230	Fig. 231	Fig. 232	Fig. 233	Fig. 234	Fig. 235	Fig. 236	Fig. 237	Fig. 238	Fig. 239	Fig. 240	Fig. 241	Fig. 242	Fig. 243	Fig. 244	Fig. 245	Fig. 246	Fig. 247	Fig. 248	Fig. 249	Fig. 250	Fig. 251	Fig. 252	Fig. 253	Fig. 254	Fig. 255	Fig. 256	Fig. 257	Fig. 258	Fig. 259	Fig. 260	Fig. 261	Fig. 262	Fig. 263	Fig. 264	Fig. 265	Fig. 266	Fig. 267	Fig. 268	Fig. 269	Fig. 270	Fig. 271	Fig. 272	Fig. 273	Fig. 274	Fig. 275	Fig. 276	Fig. 277	Fig. 278	Fig. 279	Fig. 280	Fig. 281	Fig. 282	Fig. 283	Fig. 284	Fig. 285	Fig. 286	Fig. 287	Fig. 288	Fig. 289	Fig. 290	Fig. 291	Fig. 292	Fig. 293	Fig. 294	Fig. 295	Fig. 296	Fig. 297	Fig. 298	Fig. 299	Fig. 300	Fig. 301	Fig. 302	Fig. 303	Fig. 304	Fig. 305	Fig. 306	Fig. 307	Fig. 308	Fig. 309	Fig. 310	Fig. 311	Fig. 312	Fig. 313	Fig. 314	Fig. 315	Fig. 316	Fig. 317	Fig. 318	Fig. 319	Fig. 320	Fig. 321	Fig. 322	Fig. 323	Fig. 324	Fig. 325	Fig. 326	Fig. 327	Fig. 328	Fig. 329	Fig. 330	Fig. 331	Fig. 332	Fig. 333	Fig. 334	Fig. 335	Fig. 336	Fig. 337	Fig. 338	Fig. 339	Fig. 340	Fig. 341	Fig. 342	Fig. 343	Fig. 344	Fig. 345	Fig. 346	Fig. 347	Fig. 348	Fig. 349	Fig.
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[illegible]

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNC SAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSQVVEGQWQWVDGTPLTKSLSPWDVGEPNNIATLED CATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTTVVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDR
EIDEIVIELTVQVKPVTVCVRPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIG
VLVVLAVLALITLIGICAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267